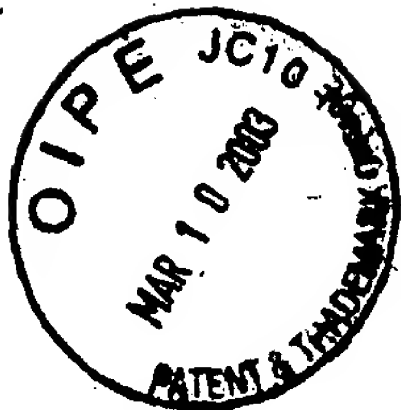


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PATENT
0147-0211P

IN THE U.S. PATENT AND TRADEMARK OFFICE

APPLICANT: Rosenthal, Andre et al. CONF: 7286
SERIAL NO.: 09/647,377 GROUP: 1632
FILED: September 27, 2000 EXAMINER: PRIEBE, S.
FOR: NUCLEIC ACID MOLECULES ENCODING PROTEINS
WHICH INFLUENCE BONE DEVELOPMENT

DECLARATION SUBMITTED UNDER 37 C.F.R. § 1.132

Honorable Commissioner
Of Patents and Trademarks
Washington, D.C. 20231

February 26, 2003

Sir:

I, Andreas Rump of the metaGen Pharmaceuticals GmbH, Germany, do hereby
declare the following:

I have attached a copy of my curriculum vitae to this Declaration.

I am Research Scientist, of the Oncology Department and have conducted the
experiments described below.

I am an co-inventor of the above referenced patent application and am familiar
with the development, usages and properties of LOBO ("long-bone") proteins described
therein.

I have read and understand the subject matter of the Office Action of September
3, 2002.

Appl. No. 09/647,377

The following comments are offered in support of the patentability of the instant invention.

I have performed two types of searches to demonstrate the similarity between the murine LOBO protein and the human homolog LOBO protein described in the instant invention. In the first search, I used LALIGN to compare both the protein and the DNA sequences of the murine and human LOBO sequences. This search was done using the complete sequence of the murine LOBO protein/DNA disclosed in the application and the partial sequence of the human as known at the time of filing as well as the complete sequence as determined after the filing date of the instant application. LALIGN compares two protein or DNA sequences for local similarity and shows the local sequence alignments. LALIGN uses code developed by X. Huang and W. Miller (Adv. Appl. Math. (1991) 12:337-357) for the "sim" program. LALIGN will report a specified number of alignments (the default is 10) between the two sequences and their scores. The results of these comparisons are attached hereto as Appendices I (comparison of the complete mouse sequences v. partial human sequences known at the time of filing) and II (comparison of the complete mouse sequences v. complete human sequences as determined after the application was filed).

The results in Appendix I indicate that the sequence identity between the LOBO Coding Sequences of the Mouse (complete) v. Man (partial) was 85.2%. The sequence identity between the Mouse (complete) v. Man (partial) in the LOBO Protein-Alignment was 88.1% and the protein sequence similarity was 94.8%. The results in Appendix II indicate that the sequence identity for the LOBO Coding Sequences of the Mouse (complete) and Man (complete) was 85.9%. The sequence identity between the Mouse (complete) and Man (complete) in the LOBO Protein-Alignment was 88.3% and the protein sequence similarity was 96.2%. The results in Appendix II which compares the Mouse (complete) to Man (complete) further demonstrates the high degree of conservation between the murine and human DNA and protein sequences.

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I also performed a BLAST search (See, Altschul, S. et al. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402) to locate similar sequences using as query the complete mouse LOBO protein sequence shown as SEQ ID No: 9 in the present application (see Annex 1; 870 amino acid residues). The blast search was done via the NCBI website (<http://www.ncbi.nlm.nih.gov/BLAST/>) against the complete translated GenBank database on January 29, 2003 (blastP). The complete results are summarized in Table 2, where the Subject ID, accession number, brief description of the subject, a bit score and e-value are listed. This list is followed by an alignment of the query and subject sequences. Each alignment indicates the percent identity and percent similarity between the two aligned sequences. Table 1 lists the ten sequences having the most significant identities.

The blastP search, Protein query-Translated db [blastP] was done using the program BLASTP 2.2.5 (version from Nov-16-2002) with the following default parameters:

- a. Databases searched: non-redundant = nr (All non-redundant GenBank CDS translations + PDB = [Sequences derived from the 3-dimensional structure from Brookhaven Protein Data Bank] + SwissProt = [Last major release of the SWISS-PROT protein sequence database (no updates)] + PIR + PRF)
- b. Limit by entrez query: No limitations were made which means all subsets of the above-cited databases were searched without any exclusions.
- c. Filter used: Low complexity. Filtering can eliminate statistically significant but biologically uninteresting reports from the blast output (e.g., hits against common acidic-, basic- or proline-rich regions), leaving the more biologically interesting regions of the query sequence available for specific matching against database sequences. Furthermore, in some cases, sequences are masked in their entirety,

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indicating that the statistical significance of any matches reported against the unfiltered query sequence should be suspect.

- d. Expect value = 10. This is the statistical significance threshold for reporting matches against database sequences. When the default value is 10, only 10 matches are expected to be found merely by chance, according to the stochastic model of Karlin and Altschul (1990). If the statistical significance ascribed to a match is greater than the EXPECT threshold, the match will not be reported. Lower EXPECT thresholds are more stringent, leading to fewer chance matches being reported. Increasing the threshold shows less stringent matches. Fractional values are acceptable.
- e. Word size = 3. This sets the size of the short regions of similarity between sequences for which BLAST initially searches.
- f. Matrix = BLOSUM62; Gap Costs: Existence = 11; Extension = 1. Here, the theory of amino acid substitution matrices is described in [1], and applied to DNA sequence comparison in [2]. In general, different substitution matrices are tailored to detecting similarities among sequences that are diverged by differing degrees [1-3]. A single matrix may nevertheless be reasonably efficient over a relatively broad range of evolutionary change [1-3]. Experimentation has shown that the BLOSUM-62 matrix [4] is among the best for detecting most weak protein similarities. For particularly long and weak alignments, the BLOSUM-45 matrix may prove superior. A detailed statistical theory for gapped alignments has not been developed, and the best gap costs to use with a given substitution matrix are determined empirically.

[1] Fitch, W.M. (1983) "Random sequences." J. Mol. Biol. 163:171-176

[2] Lipman, D.J., Wilbur, W.J., Smith T.F. & Waterman, M.S. (1984) "On the statistical significance of nucleic acid similarities." Nucl. Acids Res. 12:215-226.

[3] Altschul, S.F. & Erickson, B.W. (1985) "Significance of nucleotide sequence alignments: a method for random sequence permutation that preserves dinucleotide and codon usage." Mol. Biol. Evol. 2:526-538.

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[4] Deken, J. (1983) "Probabilistic behavior of longest-common-subsequence length." In "Time Warps, String Edits and Macromolecules: The Theory and Practice of Sequence Comparison." D. Sankoff & J.B. Kruskal (eds.), pp. 55-91, Addison-Wesley, Reading, MA.

NCBI Blast searches have for years been a routine and standard tool used by scientists for identifying similarities between sequences. The following citation from NCBI (http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html) attests to this fact: "BLAST® (Basic Local Alignment Search Tool) is a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. The BLAST programs have been designed for speed, with a minimal sacrifice of sensitivity to distant sequence relationships. The scores assigned in a BLAST search have a well-defined statistical interpretation, making real matches easier to distinguish from random background hits. BLAST uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions of similarity."

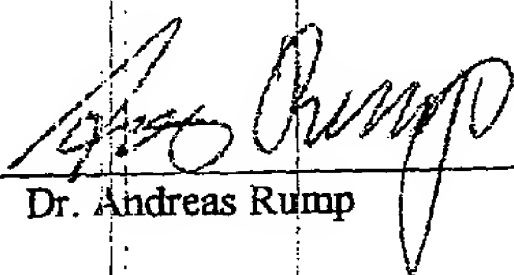
Using the above described standard blast procedure and SEQ ID No.: 9 of the present invention as a query, I obtained the following results: The hit showing the highest degree of identity in the blastP search performed was database identification No gi 25019857 (accession XP_110318.2). This protein is identified as being similar to hypothetical protein MGC37640 from *Mus musculus* and had a 97% sequence identity and a 97% sequence similarity. The murine LOBO protein of the present invention and XP_110318.2 lack identity for only 16 amino acid residues. This is likely the result of, for example, irresolvable secondary structure encountered during the sequencing process. Based on this alignment, I believe that XP_110318.2 and SEQ ID No. 9 describe one and the same sequence having equivalent functions. The nine other hits having a degree of identity greater than 70% are listed in Table 1. All of these proteins were of human or mouse origin. While the identity values for the last three sequences listed in Table 1 (Accession Nos. BAC03400.1, AAH30113.1 and XP_237349.1) have sequence identities ranging from 88% to 91%, these sequences represent a comparison of only 128-188 amino acids of the query sequences.

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The results of the blastP search are ordered by the value of % identity (see Table 2). The next "best" hit, after the 10 noted above, in the blastP search showed 37% identity to the protein sequence of SEQ ID NO.: 9. This next best hit in the blastP search has the identification No. gi 21292324 (equal to accession number EAA04469.1), which is defined as agCP3212 [*Anopheles gambiae* str. PEST]. The alignment of the polypeptide translated from gi 21292324 with SEQ ID NO.: 9 resulted in the value of 37% identity and accounted for 794 amino acid residues. In conclusion there are no proteins appearing in the blastP search having more than 70% identity to the amino acid sequence of SEQ ID NO.: 9 (murine LOBO protein).

All of the closest hits obtained in the blastP search, as identified in Table 1, were entered into the BLAST database after the filing date of the above-identified application. Furthermore, no function has been attributed to these sequences as illustrated by their descriptions, i.e. "hypothetical protein", etc. I believe that these proteins will have the same basic function as the murine LOBO protein given the significant degree of sequence identity and sequence similarity.

The undersigned hereby declares that all statements made herein based upon knowledge are true, and that all statements made based upon information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

DATED: Feb - 27 - 2003
Dr. Andreas Rump

Enclosures: As stated above



#15
4th to #15

Dr. Andreas Rump
Curriculum vitae

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Personal Details

- Date of birth: **Sept. 7, 1960**
- Place of birth: **Hamm, Germany**
- Nationality: **German**
- Family status: **married, 5 children**
- **Private Address:**
Andreas Rump, Leutraer Weg 3a, 07745 Jena
☎ +49-3641-212866
✉ andreas_rump@hotmail.com

Current place of work

- **Since December 2000**
Employed at *metaGen Pharmaceuticals*, a company dedicated to the identification of potential targets suitable for the treatment of solid tumors. Position: Scientific Leader of the "genomic technologies group"; involved in large-scale annotation of genomic DNA, cloning and expression of full-length cDNAs, DNA sequence analysis and early validation of target genes.

Previous places of work

- **January 1996 - November 2000 (5 years)**
Research Scientist at the *Institute of Molecular Biotechnology (IMB)*, *Dept. of Genome Analysis*, headed by Prof. Dr. André Rosenthal.
Areas of work: large-scale sequencing and molecular characterization of mouse mutants with defects in bone development.
- **July 1994 - December 1995 (1.5 years)**
PostDoc at the *Institute of Neuropathology* in Heidelberg, headed by Prof. Dr. Marika Kiessling.
Area of work: expression of glutamate receptors after global cerebral ischemia.

- **July 1991 – June 1994 (3 years)**
PostDoc at the *German Cancer Research Center (DKFZ)* in Heidelberg.
Department: „Interactions of carcinogens with biological macromolecules“, headed by Prof. Dr. Dr. Heinz-Walter Thielmann.
Area of work: molecular characterization of the basal cell nevus syndrome.

Postgraduate education

- **July 1987 – June 1991 (4 years)**
Ph.D. student within the *Dept. of Molecular Genetics*, at the *German National Research Center for Environment and Health (GSF)*.
Ph.D. thesis: "Molecular characterization of the pythopathogenic fungus *Phytophthora parasitica*: construction of a representative genomic cosmid library and identification of pathologically relevant genes".

Undergraduate education

- **October 1980 – June 1987 (7 years)**
Student at the Institute of Biology at the University of Bielefeld, Germany. Diploma thesis from the *Dept. of Molecular Biology and Genetics*, headed by Prof. Dr. Alfred Pühler. Title of thesis: "Nucleotide sequence of the *nifA* gene of *Klebsiella pneumoniae* M5a1".

Berlin, Feb. 21, 2003

Andreas Rump

Publications

Gene 295 (2002) 27-32

Different structural organization of the encephalopsin gene in man and mouse

Kasper G, Taudien S, Staub E, Mennerich D, Rieder M, Hinzmann B, Dahl E, Schwidetzky U, Rosenthal A, **Rump A**.

Biochem Biophys Res Comm 289 (2001) 1287-1294

Gene structure and regulation of the murine epithelial calcium channels ECaC1 and 2

Weber K, Erben RG, **Rump A**, Adamski J.

Genomics 78 (2001) 197-205

A high-resolution genetic, physical, and comparative gene map of the doublefoot (Dbf) region of mouse chromosome 1 and the region of conserved synteny on human chromosome 2q35

Hayes C, **Rump A** (shared 1st authorship), Cadman MR, Harrison M, Evans EP, Lyon MF, Morriss-Kay GM, Rosenthal A, Brown SD.

Genomics 73 (2001) 55-55

Complex arrangement of genes within a 220-kb region of double-duplicated DNA on human 2q37.1

Rump A, Kasper G, Hayes C, Wen G, Starke H, Liehr T, Lehmann R, Lagemann D, Rosenthal A.

Nature 409 (2001) 860-921

Initial sequencing and analysis of the human genome

Author list from IMB Jena: Rosenthal A, Platzer M, Nyakatura G, Taudien S, **Rump A**.

Trends in Genetics 16 (2000) 519-520

RUMMAGE – a high throughput sequence annotation system

Taudien S, **Rump A**, Platzer M, Drescher B, Schattevoy R, Gloeckner G, Dette M, Baumgart C, Weber J, Menzel U, Rosenthal A.

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Elevated DNA sequence diversity in the genomic region of the phosphatase PPP2R3L gene in the human pseudoautosomal region

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Mallon AM, Platzer M, Bate R, Gloeckner G, Botcherby MR, Nordsiek G, Strivens MA, Kioschis P, Dangel A, Cunningham D, Straw RN, Weston P, Gilbert M, Fernando S, Goodall K, Hunter G, Greystong JS, Clarke D, Kimberley C, Goerdes M, Blechschmidt K, **Rump A**, Hinzmann B, Mundy CR, Miller W, Poustka A, Herman GE, Rhodes M, Denny P, Rosenthal A, Brown SD.

Nature 405 (2000) 311-319

The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium

Hattori M, Fujiyama A, Taylor TD, Watanabe H, Yada T, Park HS, Toyoda A, Ishii K, Totoki Y, Choi DK, Soeda E, Ohki M, Takagi T, Sakaki Y, Taudien S, Blechschmidt K, Polley A, Menzel U, Delabar J, Kumpf K, Lehmann R, Patterson D, Reichwald K, **Rump A**, Schillhabel M, Schudy A. et al.

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Pseudoautosomal deletions encompassing a novel homeobox gene cause growth failure in idiopathic short stature and Turner syndrome

Rao E, Weiss B, Fukami M, **Rump A**, Niesler B, Mertz A, Muroya K, Binder G, Kirsch S, Winkelmann M, Nordsiek G, Heinrich U, Breuning MH, Ranke MB, Rosenthal A, Ogata T, Rappold GA.

J Cereb Blood Flow Metab 16 (1996) 1362-1365

Editing of GluR2 RNA in the gerbil hippocampus after global cerebral ischemia

Rump A, Sommer C, Gass P, Bele S, Meissner D, Kiessling M.

Arch Dermatol Res. 288 (1996) 399-401

Basal cell nevus syndrome and dysplastic nevus syndrome: investigation of gene expression by differential hybridisation

Rump A, Fleischmann P, Jung EG, Werner D, Thielmann HW.

Gene 102 (1991) 51-56

Tandem arrangement of tRNA(Asp)-encoding genes in Phytophthora spp.

Rump A, Karlovsky P.

J Mol Biol 203 (1988) 715-738

Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of Klebsiella pneumoniae

Arnold W, **Rump A**, Klipp W, Priefer UB, Pühler A.

Region of overlap 1521 nt; Identity [%] 85.2 %

	1120	1130	1140	1150	1160	1170
MM-LOB	AAAGACTGTATCTTCACCATTGATCCATCAACTGCTCGCGACCTTGATGATGCCCTCGCC					
	:	:	:	:	:	:
HS-Lob	AAAGACTGTATCTTCACCATTGACCCATCAACCGCCCCGAGACCTCGATGATGCCCTCTCC					
	10	20	30	40	50	60

	1180	1190	1200	1210	1220	1230
MM-LOB	TGCAGGCGGCTCACTGATGGCACCTTCGAAGTGGGCGTCCACATCGCCGATGTGAGTTAC					
	:::	::	:::	:::	:::	:::
HS-Lob	TGCAAGCCACTCGCTGACGGCAACTTCAAAGTGGGAGTTCACATTGCTGACGTGAGTTAC					
	70	80	90	100	110	120

	1240	1250	1260	1270	1280	1290
MM-LOB	TTTGTTCCTGAGGGATCCTCTTTGGATAAAGTAGCTGCTGAGAGAGCCACAAGTGTCTAC					
	::: :::	::: :::	: :::	::: :::	::: :::	::: :::
HS-Lob	TTTGTTCGGAGGGATCTGATCTGGATAAAGTGGCTGCCGAGAGGGCTACAAGCGTCTAC					
	130	140	150	160	170	180

	1300	1310	1320	1330	1340	1350'
MM-LOB	TTGGTCCAGAAAGGTGGTCCCCATGCTTCCCAGGCTTCTGTGTGAGGA	ACTCTGCAGCCTC				
	: : :	:	:	:	:	:
HS-Lob	TTGGTTCAAAGGTGGTCCCCATGCTTCCCAGGCTGCTGTGTGAGGAGCTGTGCAGCCTC					
	190	200	210	220	230	240

	1360	1370	1380	1390	1400	1410
MM-LOB	AACCCCATGACTGACAAGCTGACCTTCTCTGTGATCTGGAAGCTGACCCCTGAAGGCAAG					
	:	:	:	:	:	:
HS-Lob	AACCCCATGTCCGACAAGCTGACCTTCTCTGTGATCTGGACACTGACTCCAGAGGGCAAG					
	250	260	270	280	290	300

	1420	1430	1440	1450	1460	1470
MM-LOB	ATCCTTGAAGAGTGGTTTGGCCGCACTATCATCCGTTCTTGACCAAACCTGAGCTACGAC					
	::: ::	::: ::	::: ::	::: ::	::: ::	::: ::
HS-Lob	ATCCTTGATGAATGGTTTGGCCGACCATCATCCGCTCCTGCACCAAACCTTAGCTACGAG					
	310	320	330	340	350	360

	1480	1490	1500	1510	1520	1530
MM-LOB	CATGCCCAGAGCATGATCGAAAATCCAAGATCCCTGAGGAAGAGCTTCCCCCA					
	: : : :	: : : : : : : :	: : : :	: : : : : : : :	: : : : : :	: : : : : : : :
HS-Lob	CATGCACAGAGCATGATTGAAAGCCCAACTGAGAAAATCCCTGCGAAAGAGCTGCCCCC					
	370	380	390	400	410	420

	1540	1550	1560	1570	1580	1590
MM-LOB	ATTTCTCCAGAGCACAGCGTCGAGGAGGTGCACCAGGCAGTCCTGAACCTGCACAGCATT					
	: : : :	: : : : : :	: : :	: : : : : :	: : : : : :	: : : : : :
HS-Lob	ATTTCCCCAGAGCATAGCAGCGAGGAGGTACACCAGGCCGTCTTGAATCTCCACGGAATT					
	430	440	450	460	470	480

	1600	1610	1620	1630	1640	1650
MM-LOB	GCAAAGCAACTCCGCCGCCAGCGCTTTGTAGATGGCGCACTCCGTTTAGATCAGCTGAAG					
	:: :::: : :::: :::::::::: :: :::::::::: :::: :::::::::: :::					
HS-Lob	GCCAAGCAGTTACGCCAGCAGCGCTTTGTGGACGGCGCACTTCGTTTGATCAGCTAAAG					
	490	500	510	520	530	540

1660	1670	1680	1690	1700	1710
MM-LOB	CTTGCTTTTACTCTGGACCATGAGACTGGACTGCCTCAAGGATGTCACATCTATGAGTAC				

HS-Lob	CTTGCTTTTCACTCTGGACCACGAGACCGGATTGCCTCAAGGATGTCATATCTATGAGTAC				
	550	560	570	580	590 600

1720	1730	1740	1750	1760	1770
MM-LOB	CGAGACAGCAACAAGCTTGTAGAGGAGTTCATGCTCCTGGCCAACATGGCGGTGGCCCAC				
	:: ::	::	::	::	::
HS-Lob	CGCGAGAGCAACAAGCTCGTGGAGGAGTTCATGCTCTTGGCCAACATGGCAGTGGCCCAC				
	610	620	630	640	650 660

1780	1790	1800	1810	1820	1830
MM-LOB	AAGATCTTCCGCACCTTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCACCACAGACG				

HS-Lob	AAGATCCACCGCGCCTTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCGCCCCAAACA				
	670	680	690	700	710 720

1840	1850	1860	1870	1880	1890
MM-LOB	AAGATGCTCAGTGACCTGGTGGAGTTCTGTGACCAGATGGGGCTGCCCATGGATGTCAGC				
	:	:	:	:	:
HS-Lob	AGGATGCTCAGTGACCTGGTGGAAATTCTGCGACCAGATGGGGCTGCCCGTGGACTTCAGC				
	730	740	750	760	770 780

1900	1910	1920	1930	1940	1950
MM-LOB	TCTGCAGGGGCCCTAAATAAAAGCCTGACTAAGACATTTGGAGATGACAAGTACTCTCTG				
	::	::	::	::	::
HS-Lob	TCCGCAGGAGCCCTCAATAAAAGCCTGACCCAAACATTTGGAGATGACAAGTACTCACTG				
	790	800	810	820	830 840

1960	1970	1980	1990	2000	2010
MM-LOB	GCCCGGAAGGAGGTGCTCACCAACATGTACTCCCGGCCCATGCAGATGGCACTGTACTTC				

HS-Lob	GCCCGCAAGGAGGTGCTCACCAACATGTGCTCCCGGCCCATGCAGATGGCACTGTACTTC				
	850	860	870	880	890 900

2020	2030	2040	2050	2060	2070
MM-LOB	TGCTCTGGGATGCTGCAGGACCAGGAGCAGTTCCGGCATTATGCTCTCAACGTTCCCCTC				

HS-Lob	TGCTCGGGGCTGCTGCAGGACCCAGCGCAGTTCCGGCACTACGCGCTCAATGTGCCCCTG				
	910	920	930	940	950 960

2080	2090	2100	2110	2120	2130
MM-LOB	TACACACACTTCACCTCTCCCATCCGCCGCTTTGCTGACGTCATAGTGACCGCCTCCTG				

HS-Lob	TACACACACTTCACCTCGCCCATCCGCCGCTTTGCCGACGTCCTGGTGCACCGCCTCCTG				
	970	980	990	1000	1010 1020

2140	2150	2160	2170	2180	2190
MM-LOB	GCTGCTGCTCTGGGCTACAGTGAACAGCCAGATGTGGAGCCTGATACCCTACAGAAGCAA				

HS-Lob	GCTGCCGCGTTAGGCTATAGGGAGCGACTAGACATGGCGCCCGATACCCTGCAGAAACAG				
	1030	1040	1050	1060	1070 1080

2200	2210	2220	2230	2240	2250
MM-LOB	GCTGACCACTGCAATGACCGTCGCATGGCTTCCAAACGTGTGCAGGAGCTCAGCATCGGC				
	::	::	::	::	::
HS-Lob	GCGGACCACTGTAACGACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACCAGT				

	1090	1100	1110	1120	1130	1140
	2260	2270	2280	2290	2300	2310
MM-LOB	CTCTTCTTCGCAGTTCTAGTAAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGGTGATG					
	::::::::::	::	:::::	::	::::::::::::::::::::::::::	::::::::::::::::::
HS-Lob	CTCTTCTTTGCTGTTCTGGTCAAGGAGAGTGGCCCCCTGGAGTCAGAAGCCATGGGTGATG					
	1150	1160	1170	1180	1190	1200
	2320	2330	2340	2350	2360	2370
MM-LOB	GGTGTCTGAACCAAGCTTTTCGACGTGCTGGTGCTGCGCTTTGGGGTGCAGAAGCGCATC					
	::	::::::::::	:::::	::::::::::::::::::::::::::	::	::::::::::::::::::
HS-Lob	GGCATCTGAAGCAAGCCTTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAAGCGCATC					
	1210	1220	1230	1240	1250	1260
	2380	2390	2400	2410	2420	2430
MM-LOB	TACTGCAATGCACTGGCCCTGCGATCCTACAGCTTCCAGAAGGTGGGGAAGAAGCCAGAG					
	::::::::::	::::::::::::::::::	:::	::	::::::::::::::::::	::::::::::
HS-Lob	TACTGCAACGCACTGGCCCTGCGGTCCCACCACTTCCAGAAGGTGGGCAAGAAGCCGGAA					
	1270	1280	1290	1300	1310	1320
	2440	2450	2460	2470	2480	2490
MM-LOB	CTCACTCTTGTTTGGGAGCCTGATGACCTTGAAGAGGAGCCAACACAGCAGGTCATCACC					
	:::::	::	::	::::::::::	:::	:
HS-Lob	CTCACGCTGGTCTGGGAGCCTGAGGACATGGAGCAGGAGCCAGCACAGCAGGTCATCACC					
	1330	1340	1350	1360	1370	1380
	2500	2510	2520	2530	2540	2550
MM-LOB	ATCTTCAGCCTGGTGGATGTGGTCCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCT					
	::::::::::::::::::	::::::::::::::::::	::::::::::::::::::	::::::::::::::::::	::::::::::::::::::	::
HS-Lob	ATCTTCAGCCTGGTGGAGGTGGTCCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCC					
	1390	1400	1410	1420	1430	1440
	2560	2570		2580		2590
MM-LOB	ATCCTGAAGCGACCAGGC-----CTGG-----AGAAGGCGTCT					
	::::::::::	:::::		::::		::
HS-Lob	ATCCTGAAGCGGCCAGGCACCCAGGGCCACCTGGGCCCCTGAGAAGGAGGAGGAGTCT					
	1450	1460	1470	1480	1490	1500
	2600	2610				
MM-LOB	GATGAGGAGCCTGAGGACTGA					
	::	:	:::::	:::::	:	:
HS-Lob	GACGGTGAGCCCGAGGACTCA					
	1510	1520				

LOBO Protein-Alignment: Mouse (complete) vs. Man (partial, as known at the time of patent filing)

Region of overlap 506 aa; Identity [:] 88.1 %; Similarity [.] 94.8 %

Program used: LALIGN (rigorous local alignment)

```

      380      390      400      410      420      430
MM-LOB KDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFVPEGSSLDKVAAERATSVY
      .....
HS-LOB KDCIFTIDPSTARDLDDALSCPLADGNFKVGVHIADVSFVPEGSDLDKVAAERATSVY
      10      20      30      40      50      60

      440      450      460      470      480      490
MM-LOB LVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYD
      .....
HS-LOB LVQKVVPMLPRLLCEELCSLNPMSDKLTFSVIWTLTPEGKILDEWFGRTIIRSCTKLSYE
      70      80      90      100      110      120

      500      510      520      530      540      550
MM-LOB HAQSMIENPTEKIPPEELPPISPEHSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLK
      .....
HS-LOB HAQSMIESPTEKIPAKELPPISPEHSSEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLK
      130      140      150      160      170      180

      560      570      580      590      600      610
MM-LOB LAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQT
      .....
HS-LOB LAFTLDHETGLPQGCHIYEYRESNKLVEEFMLLANMAVAHKIHRAFPEQALLRRHPPPQT
      190      200      210      220      230      240

      620      630      640      650      660      670
MM-LOB KMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYF
      .....
HS-LOB RMLSDLVEFCDQMGLPVDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMCSRPMQMALYF
      250      260      270      280      290      300

      680      690      700      710      720      730
MM-LOB CSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQ
      .....
HS-LOB CSGLLQDPAQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYRERLDMAPDTLQKQ
      310      320      330      340      350      360

      740      750      760      770      780      790
MM-LOB ADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRI
      .....
HS-LOB ADHCNDRRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQAFDVLVLRFGVQKRI
      370      380      390      400      410      420

      800      810      820      830      840      850
MM-LOB YCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATAALKYSA
      .....
HS-LOB YCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPAQVITIFSLVEVVLQAEATAALKYSA
      430      440      450      460      470      480

      860      870
MM-LOB ILKRPGL-----EKASDEEPED
      .....
HS-LOB ILKRPGTQGHGPEKEEEESDGEPE
      490      500
```

APPENDIX II

LOBO Protein-Alignment: Mouse (complete) vs. Man (complete, as determined after patent filing)

Region of overlap 881 aa; Identity [:] 88.3 %; Similarity [.] 96.2 %

Program used: LALIGN (rigorous local alignment)

	10	20	30	40	50	60
MM-LOB	MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS	MRGKKKSI	FETYMSKEDVS			

HS-LOB	MSHPDYRMNLRPLGTPRGVSAVAGPHDIGASPGDKKSKNRSTRGKKKSI	FETYMSKEDVS				
	10	20	30	40	50	60
	70	80	90	100	110	120
MM-LOB	EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGD	DRDIFIDGVVARNRALNGDLVVKLLPEDQ				

HS-LOB	EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGD	DRDIFIDGVVARNRALNGDLVVKLLPEEH				
	70	80	90	100	110	120
	130	140	150	160	170	
MM-LOB	WKA	VPESNDKEIEATYEADIPEEGCGHHPLQ	QSRKGS	-GPDVII	EAQFDDSDSEDRHG	

HS-LOB	WKV	VPESNDKETEAAYESDIPEELCGHHLPQ	QSLKSYNDSPDVIVEAQFDGSDSEDGHG			
	130	140	150	160	170	180
	180	190	200	210	220	230
MM-LOB	NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPI	PDTRGLSEKSLQKSAKV	VYILE			

HS-LOB	ITQNV	LVDGVKKLSVCVSEKGREDDAPVT	KDETTTCISQDTRALSEKSLQKSAKV	VYILE		
	190	200	210	220	230	240
	240	250	260	270	280	290
MM-LOB	KKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTL					

HS-LOB	KKHSRAATGFLKLLADKNSDLFRKYALFSPSDHRVPRIYVPLKDCPQDFVARPKDYANTL					
	250	260	270	280	290	300
	300	310	320	330	340	350
MM-LOB	FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLP					

HS-LOB	FICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQGLP					
	310	320	330	340	350	360
	360	370	380	390	400	410
MM-LOB	WTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFE	VGVIADVS	YFVPEG			

HS-LOB	WTIPPEEFSKRRDLRKDCIFTIDPSTARDLDDALSCKPLADGNFKVGVIADVS	YFVPEG				
	370	380	390	400	410	420
	420	430	440	450	460	470
MM-LOB	SSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM	TDKLTFSVIWKL	TPEGKILEEW			

HS-LOB	SDLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM	SDKLTFSVIWTL	TPEGKILDEW			
	430	440	450	460	470	480
	480	490	500	510	520	530
MM-LOB	FGRTIIRSCTKLSYDHAQSMIENPTEKIP	EEELPPISPEHSVEEVHQAVLN	LH	SI	AKQLR	

HS-LOB	FGRTIIRSCTKLSYEHQAQSMIESPTEKIP	AKELPPISPEHSSEEVHQAVLN	LH	GI	AKQLR	
	490	500	510	520	530	540

	540	550	560	570	580	590
MM-LOB	RQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRT					
HS-LOB	QQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRESNKLVEEFMLLANMAVAHKIHRA					
	550	560	570	580	590	600
MM-LOB	FPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEV					
HS-LOB	FPEQALLRRHPPPQTRMLSDLVEFCDQMGLPVDSSAGALNKSLTQTFGDDKYSLARKEV					
	610	620	630	640	650	660
MM-LOB	LTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG					
HS-LOB	LTNMCSRPMQMALYFCSGLLQDPAQFRHYALNVPLYTHFTSPIRRFADVLVHRLLAALG					
	670	680	690	700	710	720
MM-LOB	YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQ					
HS-LOB	YRERLDMAPDTLQKQADHCNDRRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQ					
	730	740	750	760	770	780
MM-LOB	AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLV					
HS-LOB	AFDVLVLRYGQKRIYCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPAAQQVITIFSLV					
	790	800	810	820	830	840
MM-LOB	DVLQAEATAALKYSAILKRPGLEKASDEEPED					
HS-LOB	EVLQAEATAALKYSAILKRPGTQGHLGPEKEEEESDGEPE					
	850	860	870	880		

LOBO coding sequence (CDS)-alignment: Mouse (complete) vs. Man (complete, as determined after patent filing)

	10	20	30	40	50	60
MM-LOB	ATGAACCATCCTGACTACAAGCTGAACCTTCGGTCTCCGGGGACCCCCAGAGGTGTGTCC					

HS-Lob	ATGAGCCATCCTGACTACAGAATGAACCTCCGGCCCCTGGGGACCCCCAGAGGTGTGTCT					
	10	20	30	40	50	60
	70	80	90	100	110	120
MM-LOB	TCTGTGGTTGGCCCGAGTGCTGTTGGTGCTTCGCCAGGTGACAAAAAGTCAAAGAACAAG					

HS-Lob	GCTGTGGCTGGTCCACATGACATTGGTGCTTCGCCAGGTGACAAAAAGTCAAAGAACAAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
MM-LOB	TCCATGCGAGGGAAGAAAAAGAGCATATTTGAAACCTACATGTCCAAGGAGGATGTTTCA					

HS-Lob	TCCACACGAGGGAAGAAAAAGAGCATATTTGAAACTTACATGTCCAAGGAGGATGTTTCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
MM-LOB	GAAGGCTTGAAGAGAGGAACACTTATCCAGGGTGTATTGAGAATCAACCCAAAGAAGTTT					

HS-Lob	GAAGGCTTGAAGAGAGGAACACTCATCCAGGGTGTATTGAGAATTAATCCAAAGAAGTTT					
	190	200	210	220	230	240
	250	260	270	280	290	300
MM-LOB	CATGAAGCCTTCATTCCTTCTCCGGATGGTGATCGGGACATTTTTTATTGATGGAGTTGTT					

HS-Lob	CATGAAGCCTTCATTCCTTCCCCGGATGGTGATCGAGACATTTTTTATTGATGGGGTTGTT					
	250	260	270	280	290	300
	310	320	330	340	350	360
MM-LOB	GCTCGTAATAGAGCCTTAAATGGGGACCTTGTGGTTGTAAACTGCTTCCTGAGGATCAG					

HS-Lob	GCTCGTAATAGAGCCTTAAATGGGGATCTGGTGGTCGTGAAACTGCTTCCCGAGGAGCAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
MM-LOB	TGGAAGGCAGTTAAACCAGAGAGCAATGACAAAGAAATAGAAGCTACTTATGAAGCTGAC					

HS-Lob	TGGAAGGTAGTTAAACCAGAGAGCAATGACAAAGAAACAGAAGCTGCGTATGAATCAGAT					
	370	380	390	400	410	420
	430	440	450	460	470	
MM-LOB	ATCCCTGAAGAGGGCTGTGGACATCACCCCCTGCAGCAGTCCCGGAAAGGCTGGAGTG--					

HS-Lob	ATCCCCGAGGAGCTCTGTGGACACCATCTCCCGCAACAGTCCCTGAAAAGCTATAATGAC					
	430	440	450	460	470	480
	480	490	500	510	520	530
MM-LOB	-GTCCTGATGTCATTATAGAGGCTCAGTTTGATGACAGCGACTCAGAAGATAGACATGGC					

HS-Lob	AGTCCTGATGTCATTGTAGAGGCTCAGTTTGATGGCAGCGACTCAGAAGATGGACATGGC					
	490	500	510	520	530	540

	540	550	560	570	580	590
MM-LOB	AACACC---AGTGGCCTGGTTGATGGTGTAAAGAAATTGTCAATCTCTACTCCTGACAGA					
	:	:	:	:	:	:
HS-Lob	ATCACACAAAATGTGCTGGTTGATGGTGTAAAGAACTCTCAGTTTGTGTTTCTGAGAAA					
	550	560	570	580	590	600

	600	610	620	630	640	650
MM-LOB	GGAAAAGAAGATTCTAGTACTCCAGTTATGAAAGATGAGAACACCCCCATACCACAGGAC					
	:	:	:	:	:	:
HS-Lob	GGAAGAGAGGATGGTGATGCACCGTTACAAAAGATGAGACCACCTGCATTTCACAAGAC					
	610	620	630	640	650	660

	660	670	680	690	700	710
MM-LOB	ACAAGAGGCTTATCAGAGAAGTCACTTCAGAAATCAGCAAAGGTGGTTTACATCTTGGAG					
	:	:	:	:	:	:
HS-Lob	ACAAGAGCTTTATCGGAGAAATCCCTGCAAAGATCAGCAAAGGTGGTTTACATCTTGGAG					
	670	680	690	700	710	720

	720	730	740	750	760	770
MM-LOB	AAAAAGCATTCTCGAGCAGCAACTGGCATCCTGAAACTCTTGGCTGATAAGAACAGTGAC					
	:	:	:	:	:	:
HS-Lob	AAAAACATTCTCGAGCAGCAACCGGCTTCCTCAAACCTCTTGGCTGATAAGAACAGCGAA					
	730	740	750	760	770	780

	780	790	800	810	820	830
MM-LOB	CTGTTTAAAGAAATACGCCCTGTTTTCTCCTTCAGACCACCGAGTACCTAGAATTTACGTA					
	:	:	:	:	:	:
HS-Lob	CTGTTTAGGAAATACGCCCTGTTTTCTCCCTCAGACCACCGAGTGCCTAGAATTTATGTG					
	790	800	810	820	830	840

	840	850	860	870	880	890
MM-LOB	CCTCTCAAGGACTGTCCCCAGGACTTCATGACCCGACCTAAAGACTTTGCCAACACGCTG					
	:	:	:	:	:	:
HS-Lob	CCTCTCAAGGACTGTCCCCAGGACTTTGTGGCAGGCCTAAAGATTATGCCAACACACTG					
	850	860	870	880	890	900

	900	910	920	930	940	950
MM-LOB	TTCATCTGCCGCATCATAGACTGGAAGGAGGACTGTAATTTTGCCCTGGGGCAACTGGCT					
	:	:	:	:	:	:
HS-Lob	TTCATCTGCCGCATTGTGGACTGGAAGGAGGACTGCAATTTTGCCCTGGGGCAGCTGGCT					
	910	920	930	940	950	960

	960	970	980	990	1000	1010
MM-LOB	AAGAGTCTTGGGCAGGCTGGTGAAATCGAGCCTGAAACAGAAGGGATACTGACAGAATAT					
	:	:	:	:	:	:
HS-Lob	AAGAGTCTTGGGCAGGCTGGTGAAATTGAGCCTGAAACAGAAGGAATACTAACAGAGTAT					
	970	980	990	1000	1010	1020

	1020	1030	1040	1050	1060	1070
MM-LOB	GGTGTGGACTTCTCTGATTTCTCTTCAGAAAGTTCTTGAATGTCTCCCTCAAAGCCTGCCC					
	:	:	:	:	:	:
HS-Lob	GGCGTGGATTTCTCTGATTTCTCTTCAGAAAGTTCTAGAATGTCTTCCTCAAGGCCTGCCA					
	1030	1040	1050	1060	1070	1080

	1080	1090	1100	1110	1120	1130
MM-LOB	TGGACAATCCCACCTGATGAGGTGGGCAAGAGAAGAGACCTAAGGAAAGACTGTATCTTC					

HS-Lob	TGGACAATTCCACCAGAGGAGTTCAGCAAGAGAAGGGATTTAAGAAAAGACTGTATCTTC					
	1090	1100	1110	1120	1130	1140

	1140	1150	1160	1170	1180	1190
MM-LOB	ACCATTGATCCATCAACTGCTCGCGACCTTGATGATGCCCTCGCCTGCAGGCGGCTCACT					

HS-Lob	ACCATTGACCCATCAACCGCCCGAGACCTCGATGATGCCCTCTCCTGCAAGCCACTCGCT					
	1150	1160	1170	1180	1190	1200

	1200	1210	1220	1230	1240	1250
MM-LOB	GATGGCACCTTCGAAGTGGGCGTCCACATCGCCGATGTGAGTTACTTTGTTCTGAGGGA					
	::
HS-Lob	GACGGCAACTTCAAAGTGGGAGTTCACATTGCTGACGTGAGTTACTTTGTTCCGGAGGGA					
	1210	1220	1230	1240	1250	1260

	1260	1270	1280	1290	1300	1310
MM-LOB	TCCTCTTTGGATAAAGTAGCTGCTGAGAGAGCCACAAGTGTCTACTTGGTCCAGAAGGTG					
	::
HS-Lob	TCTGATCTGGATAAAGTGGCTGCCGAGAGGGCTACAAGCGTCTACTTGGTTCAAAGGTG					
	1270	1280	1290	1300	1310	1320

	1320	1330	1340	1350	1360	1370
MM-LOB	GTCCCCATGCTTCCCAGGCTTCTGTGTGAGGAACTCTGCAGCCTCAACCCCATGACTGAC					

HS-Lob	GTCCCCATGCTTCCCAGGCTGCTGTGTGAGGAGCTGTGCAGCCTCAACCCCATGTCCGAC					
	1330	1340	1350	1360	1370	1380

	1380	1390	1400	1410	1420	1430
MM-LOB	AAGCTGACCTTCTCTGTGATCTGGAAGCTGACCCCTGAAGGCAAGATCCTTGAAGAGTGG					

HS-Lob	AAGCTGACCTTCTCTGTGATCTGGACACTGACTCCAGAGGGCAAGATCCTTGATGAATGG					
	1390	1400	1410	1420	1430	1440

	1440	1450	1460	1470	1480	1490
MM-LOB	TTTGGCCGCACTATCATCCGTTCTTGACCAAAGTACGAGCTACGACCATGCCAGAGCATG					

HS-Lob	TTTGGCCGCACTATCATCCGCTCCTGCACCAAAGTACGAGCTACGAGCATGCACAGAGCATG					
	1450	1460	1470	1480	1490	1500

	1500	1510	1520	1530	1540	1550
MM-LOB	ATCGAAAATCCAAGTGAAGATCCCTGAGGAAGAGCTTCCCCCAATTTCTCCAGAGCAC					
	::
HS-Lob	ATTGAAAGCCCAAGTGAAGAAATCCCTGCGAAAGAGCTGCCCCCATTTCCCCAGAGCAT					
	1510	1520	1530	1540	1550	1560

	1560	1570	1580	1590	1600	1610
MM-LOB	AGCGTCGAGGAGGTGCACCAGGCGTCTGAACCTGCACAGCATTGCAAAGCAACTCCGC					
	::
HS-Lob	AGCAGCGAGGAGGTACACCAGGCGTCTTGAATCTCCACGGAATTGCCAAGCAGTTACGC					
	1570	1580	1590	1600	1610	1620

	1620	1630	1640	1650	1660	1670
MM-LOB	CGCCAGCGCTTTGTAGATGGCGCACTCCGTTTAGATCAGCTGAAGCTTGCTTTTACTCTG					
	:
HS-Lob	CAGCAGCGCTTTGTGGACGGCGCACTTCGTTTGGATCAGCTAAAGCTTGCTTTTACTCTG					
	1630	1640	1650	1660	1670	1680

	1680	1690	1700	1710	1720	1730
MM-LOB	GACCATGAGACTGGACTGCCTCAAGGATGTCACATCTATGAGTACCGAGACAGCAACAAG					

HS-Lob	GACCACGAGACCGGATTGCCTCAAGGATGTCATATCTATGAGTACCGCGAGAGCAACAAG					
	1690	1700	1710	1720	1730	1740
	1740	1750	1760	1770	1780	1790
MM-LOB	CTTGTAAGAGGAGTTCATGCTCCTGGCCAACATGGCGGTGGCCCACAAGATCTTCCGCACC					

HS-Lob	CTCGTGGAGGAGTTCATGCTCTTGGCCAACATGGCAGTGGCCCACAAGATCCACCGCGCC					
	1750	1760	1770	1780	1790	1800
	1800	1810	1820	1830	1840	1850
MM-LOB	TTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCACCACAGACGAAGATGCTCAGTGAC					

HS-Lob	TTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCGCCCCAAACAAGGATGCTCAGTGAC					
	1810	1820	1830	1840	1850	1860
	1860	1870	1880	1890	1900	1910
MM-LOB	CTGGTGGAGTTCTGTGACCAGATGGGGCTGCCCATGGATGTCAGCTCTGCAGGGGCCCTA					

HS-Lob	CTGGTGGGAATTCTGCGACCAGATGGGGCTGCCCGTGGACTTCAGCTCCGCAGGAGCCCTC					
	1870	1880	1890	1900	1910	1920
	1920	1930	1940	1950	1960	1970
MM-LOB	AATAAAAGCCTGACTAAGACATTTGGAGATGACAAGTACTCTCTGGCCCCGAAGGAGGTG					

HS-Lob	AATAAAAGCCTGACCCAAACATTTGGAGATGACAAGTACTCACTGGCCCCGCAAGGAGGTG					
	1930	1940	1950	1960	1970	1980
	1980	1990	2000	2010	2020	2030
MM-LOB	CTCACCAACATGTACTCCCGGCCCATGCAGATGGCACTGTACTTCTGCTCTGGGATGCTG					

HS-Lob	CTCACCAACATGTGCTCCCGGCCCATGCAGATGGCACTGTACTTCTGCTCGGGGCTGCTG					
	1990	2000	2010	2020	2030	2040
	2040	2050	2060	2070	2080	2090
MM-LOB	CAGGACCAGGAGCAGTTCGGGCATTATGCTCTCAACGTTCCCCTCTACACACACTTCACC					

HS-Lob	CAGGACCCAGCGCAGTTCGGGCACTACGCGCTCAATGTGCCCTGTACACACACTTCACC					
	2050	2060	2070	2080	2090	2100
	2100	2110	2120	2130	2140	2150
MM-LOB	TCTCCCATCCGCCGCTTTGCTGACGTCATAGTGCACCGCCTCCTGGCTGCTGCTCTGGGC					

HS-Lob	TCGCCCATCCGCCGCTTTGCCGACGTCCTGGTGCACCGCCTCCTGGCTGCCGCGTTAGGC					
	2110	2120	2130	2140	2150	2160
	2160	2170	2180	2190	2200	2210
MM-LOB	TACAGTGAACAGCCAGATGTGGAGCCTGATACCCTACAGAAGCAAGCTGACCACTGCAAT					

HS-Lob	TATAGGGAGCGACTAGACATGGCGCCCGATACCCTGCAGAAACAGGCGGACCACTGTAAC					
	2170	2180	2190	2200	2210	2220

2220 2230 2240 2250 2260 2270
MM-LOB GACCGTCGCATGGCTTCCAAACGTGTGCAGGAGCTCAGCATCGGCCTCTTCTTCGCAGTT
 :
HS-Lob GACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACCAGTCTCTTCTTTGCTGTT
 2230 2240 2250 2260 2270 2280

2280 2290 2300 2310 2320 2330
MM-LOB CTAGTAAAGGAGAGTGCCCCCTGGAGTCCGAAGCCATGGTGATGGGTGTCCTGAACCAA
 :
HS-Lob CTGGTCAAGGAGAGTGCCCCCTGGAGTCAGAAGCCATGGTGATGGGCATCCTGAAGCAA
 2290 2300 2310 2320 2330 2340

2340 2350 2360 2370 2380 2390
MM-LOB GCTTTCGACGTGCTGGTGCTGCGCTTTGGGGTGCAGAAGCGCATCTACTGCAATGCACTG
 :
HS-Lob GCCTTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAAGCGCATCTACTGCAACGCACTG
 2350 2360 2370 2380 2390 2400

2400 2410 2420 2430 2440 2450
MM-LOB GCCCTGCGATCCTACAGCTTCCAGAAGGTGGGGAAGAAGCCAGAGCTCACTCTTGTTTGG
 :
HS-Lob GCCCTGCGGTCCCACCACTTCCAGAAGGTGGGCAAGAAGCCGGA ACTCACGCTGGTCTGG
 2410 2420 2430 2440 2450 2460

2460 2470 2480 2490 2500 2510
MM-LOB GAGCCTGATGACCTTGAAGAGGAGCCAACACAGCAGGTCATCACCATCTTCAGCCTGGTG
 :
HS-Lob GAGCCTGAGGACATGGAGCAGGAGCCAGCACAGCAGGTCATCACCATCTTCAGCCTGGTG
 2470 2480 2490 2500 2510 2520

2520 2530 2540 2550 2560 2570
MM-LOB GATGTGGTCCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCTATCCTGAAGCGACCA
 :
HS-Lob GAGGTGGTCCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCCATCCTGAAGCGGCCA
 2530 2540 2550 2560 2570 2580

 2580 2590 2600
MM-LOB GGC-----CTGG-----AGAAGGCGTCTGATGAGGAGCCTGAG
 :
HS-Lob GGCACCCAGGGCCACCTGGGCCCTGAGAAGGAGGAGGAGGAGTCTGACGGTGAGCCCGAG
 2590 2600 2610 2620 2630 2640

2610
MM-LOB GACTGA
 : : : : :
HS-Lob GACTCA

TABLE 1

Blast of **complete mouse LOBO protein** against translated GenBank produced hits with significant similarity with the following DB-entries (Blast performed 30-Jan-2003):

All other matches were significantly lower than 70 % aa identity

RESULT: no entry with significant (i.e. >70 % aa identity) was older than May 2002 !!

Similarity	Accession	Entry date	Remark
818/870 (94%)	NP_705758.1	26-JAN-2003	
801/831 (96%)	BAC27292.1	05-DEC-2002	
720/772 (93%)	XP_129937.2	16-NOV-2002	version 1: 08-OCT-2002
647/663 (97%)	XP_110318.2	15-NOV-2002	version 1: 30-APR-2002
569/590 (96%)	BAC26549.1	05-DEC-2002	
451/532 (84%)	AAH36113.1	23-SEP-2002	
410/527 (77%)	BAC04324.1	15-JUL-2002	
167/188 (88%)	BAC03400.1	15-JUL-2002	
119/135 (88%)	AAH30113.1	20-MAY-2002	
117/128 (91%)	XP_237349.1	28-JAN-2003	

TABLE 2

The detailed Blast results are as follows:

BLASTP 2.2.5 [version from Nov-16-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1043949663-07491-641

Query= MM-LOBO 871 bp PROT 6-NOV-1998,
871 bases, 670 checksum.
(870 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,321,324 sequences; 423,161,544 total letters

Sequences producing significant alignments:				Score (bits)	E Value
gi 24233556 ref NP_705758.1	RIKEN cDNA 4930429A22; hypothe...	1640	0.0		
gi 26327097 dbj BAC27292.1	unnamed protein product [Mus mu...	1605	0.0		
gi 25047588 ref XP_129937.2	hypothetical protein MGC37640 ...	1453	0.0		
gi 25019857 ref XP_110318.2	similar to hypothetical protei...	1303	0.0		
gi 26325590 dbj BAC26549.1	unnamed protein product [Mus mu...	1166	0.0		
gi 23271317 gb AAH36113.1	Unknown (protein for MGC:33943) ...	916	0.0		
gi 21753324 dbj BAC04324.1	unnamed protein product [Homo s...	812	0.0		
gi 21292324 gb EAA04469.1	agCP3212 [Anopheles gambiae str....	424	e-117		
gi 19115422 ref NP_594510.1	ribonuclease II RNB family pro...	418	e-115		
gi 15220899 ref NP_177891.1	putative 3'-5' exoribonuclease...	414	e-114		

gi	25406521	pir	E96806	hypothetical protein T32E8.1 [impor...	402	e-110
gi	25332397	pir	A84553	probable mitotic control protein di...	396	e-109
gi	24654592	ref	NP_728490.1	CG16940-PC [Drosophila melanog...	367	e-100
gi	19922976	ref	NP_612012.1	CG16940-PA [Drosophila melanog...	367	e-100
gi	15292611	gb	AAK93574.1	SD10981p [Drosophila melanogaster]	351	2e-95
gi	18488261	ref	XP_081229.1	Dis3 [Drosophila melanogaster]...	350	6e-95
gi	21748526	dbj	BAC03400.1	FLJ00327 protein [Homo sapiens]	343	9e-93
gi	26327903	dbj	BAC27692.1	unnamed protein product [Mus mu...	340	7e-92
gi	13446610	emb	CAC35051.1	putative exoribonuclease DIS3 [...	335	2e-90
gi	5262619	emb	CAB45749.1	hypothetical protein [Homo sapiens]	334	4e-90
gi	27703387	ref	XP_224449.1	similar to mitotic control pro...	330	7e-89
gi	19923416	ref	NP_055768.2	mitotic control protein dis3 h...	330	7e-89
gi	6324552	ref	NP_014621.1	Possible component of RCC1-Ran ...	321	3e-86
gi	21297331	gb	EAA09476.1	ebiP3704 [Anopheles gambiae str....	313	6e-84
gi	14250908	emb	CAC39259.1	Rrp44p homologue [Trypanosoma b...	313	1e-83
gi	19113445	ref	NP_596653.1	mitotic control protein dis3 [...	301	4e-80
gi	15021874	dbj	BAB62212.1	hypothetical protein [Macaca fa...	291	3e-77
gi	19115966	ref	NP_588616.1	hypothetical protein MGC4562 [...	284	4e-75
gi	18916779	dbj	BAB85541.1	KIAA1955 protein [Homo sapiens]	284	5e-75
gi	27369724	ref	NP_766107.1	hypothetical protein 4932411M1...	283	9e-75
gi	14250916	emb	CAC39263.1	putative ribonuclease II-like p...	278	4e-73
gi	15559519	gb	AAH14124.1	AAH14124 Unknown (protein for IMA...	270	1e-70
gi	23136616	gb	ZP_00118334.1	hypothetical protein [Cytopha...	265	3e-69
gi	19173030	ref	NP_597581.1	similarity to DIS3 PROTEIN (RN...	260	6e-68
gi	7493807	pir	T30524	protein phosphatase Ssd1 homolog - y...	246	1e-63
gi	22748821	ref	NP_689596.1	hypothetical protein MGC42174 ...	242	2e-62
gi	27685983	ref	XP_237349.1	similar to hypothetical protei...	241	5e-62
gi	6320499	ref	NP_010579.1	Product of gene unknown; Ssd1p ...	221	3e-56
gi	15616115	ref	NP_244420.1	ribonuclease R; virulence-asso...	214	5e-54
gi	23099883	ref	NP_693349.1	ribonuclease R [Oceanobacillus ...	209	1e-52
gi	21673344	ref	NP_661409.1	ribonuclease II family protein...	208	4e-52
gi	15672924	ref	NP_267098.1	ribonuclease [Lactococcus lact...	206	9e-52
gi	21754656	dbj	BAC04542.1	unnamed protein product [Homo s...	205	3e-51
gi	23020108	gb	ZP_00059814.1	hypothetical protein [Clostri...	203	1e-50
gi	16801605	ref	NP_471873.1	similar to exoribonuclease RNA...	201	3e-50
gi	16804487	ref	NP_465972.1	similar to exoribonuclease RNA...	200	7e-50
gi	21397569	ref	NP_653554.1	RNB, RNB-like protein [Bacillu...	197	7e-49
gi	16080414	ref	NP_391241.1	similar to hypothetical protei...	195	3e-48
gi	15894003	ref	NP_347352.1	FUSION ribonuclease and riboso...	190	7e-47
gi	27467483	ref	NP_764120.1	ribonuclease R [Staphylococcus...	190	8e-47
gi	24379988	ref	NP_721943.1	putative exoribonuclease R (RN...	190	1e-46
gi	19113103	ref	NP_596311.1	hypothetical protein; ribonucl...	188	3e-46
gi	21282471	ref	NP_645559.1	ribonuclease R [Staphylococcus...	187	7e-46
gi	15923770	ref	NP_371304.1	conserved hypothetical protein...	186	1e-45
gi	27685919	ref	XP_217466.1	similar to hypothetical protei...	186	2e-45
gi	6473411	dbj	BAA87129.1	Hypothetical protein [Schizosacc...	186	2e-45
gi	15926457	ref	NP_373990.1	ribonuclease R [Staphylococcus...	185	3e-45
gi	19745621	ref	NP_606757.1	putative exoribonuclease R [St...	185	3e-45
gi	15674608	ref	NP_268782.1	putative exoribonuclease R [St...	184	6e-45
gi	21909888	ref	NP_664156.1	putative exoribonuclease R [St...	183	9e-45
gi	25011590	ref	NP_735985.1	Unknown [Streptococcus agalact...	183	1e-44
gi	27685993	ref	XP_237351.1	similar to hypothetical protei...	183	1e-44
gi	22537625	ref	NP_688476.1	exoribonuclease, VacB/Rnb fami...	183	1e-44
gi	15902922	ref	NP_358472.1	Exoribonuclease R [Streptococc...	182	2e-44
gi	15900852	ref	NP_345456.1	exoribonuclease, VacB/Rnb fami...	181	3e-44
gi	15673187	ref	NP_267361.1	ribonuclease [Lactococcus lact...	179	1e-43
gi	15805382	ref	NP_294076.1	ribonuclease [Deinococcus radi...	176	2e-42
gi	15605122	ref	NP_219907.1	Ribonuclease Family [Chlamydia...	172	3e-41
gi	15618415	ref	NP_224700.1	ribonuclease family [Chlamydo...	170	1e-40
gi	20807463	ref	NP_622634.1	Exoribonucleases [Thermoanaero...	169	2e-40
gi	23024105	gb	ZP_00063328.1	hypothetical protein [Leucono...	169	2e-40
gi	27380223	ref	NP_771752.1	exoribonuclease [Bradyrhizobi...	167	6e-40
gi	15835291	ref	NP_297050.1	exoribonuclease, VacB/Rnb fami...	167	9e-40
gi	23053471	gb	ZP_00079680.1	hypothetical protein [Geobact...	166	2e-39
gi	20881074	ref	XP_127907.1	RIKEN cDNA 2810028N01 [Mus mus...	163	1e-38

gi 20071792 gb AAH27357.1	Similar to mitotic control prote...	163	1e-38
gi 15643485 ref NP_228531.1	vacB protein [Thermotoga marit...	162	2e-38
gi 23467938 gb ZP_00123514.1	hypothetical protein [Haemoph...	161	4e-38
gi 15607021 ref NP_214403.1	VacB protein (ribonuclease II ...	160	7e-38
gi 19703943 ref NP_603505.1	Exoribonuclease II [Fusobacter...	160	8e-38
gi 18310278 ref NP_562212.1	ribonuclease R [Clostridium pe...	160	1e-37
gi 23038196 gb ZP_00070371.1	hypothetical protein [Oenococ...	159	1e-37
gi 15642594 ref NP_232227.1	ribonuclease R [Vibrio cholera...	159	2e-37
gi 17545947 ref NP_519349.1	PROBABLE EXORIBONUCLEASE RNASE...	158	5e-37
gi 22995402 gb ZP_00039879.1	hypothetical protein [Xylella...	157	8e-37
gi 16763187 ref NP_458804.1	ribonuclease R (RNase R) [Salm...	157	8e-37
gi 22954374 gb ZP_00002175.1	hypothetical protein [Nitroso...	156	1e-36
gi 16132001 ref NP_418600.1	putative enzyme [Escherichia c...	156	1e-36
gi 15804768 ref NP_290809.1	putative enzyme [Escherichia c...	156	1e-36
gi 731093 sp P21499 RNR_ECOLI	Ribonuclease R (RNase R) (Vac...	156	1e-36
gi 391901 dbj BAA01777.1	ORF-2 [Shigella flexneri]	155	2e-36
gi 24115534 ref NP_710044.1	putative enzyme [Shigella flex...	155	2e-36
gi 27735249 sp P30851 RNR_SHIFL	Ribonuclease R (RNase R) (V...	155	2e-36
gi 26553786 ref NP_757720.1	3'-5' exoribonuclease RNase R ...	155	2e-36
gi 27364704 ref NP_760232.1	Exoribonuclease R [Vibrio vuln...	154	5e-36
gi 21242317 ref NP_641899.1	RNase R [Xanthomonas axonopodi...	154	5e-36
gi 15600130 ref NP_253624.1	exoribonuclease RNase R [Pseud...	154	5e-36
gi 23003758 gb ZP_00047408.1	hypothetical protein [Lactoba...	154	6e-36
gi 26251071 ref NP_757111.1	Ribonuclease R [Escherichia co...	154	6e-36
gi 11359056 pir T45283	growth polarity maintenance protein...	154	7e-36

Alignments

>gi|24233556|ref|NP_705758.1| RIKEN cDNA 4930429A22; hypothetical protein MGC37640 [Mus musculus]
 gi|23273603|gb|AAH36177.1| Unknown (protein for MGC:37640) [Mus musculus]
 Length = 870

Score = 1640 bits (4247), Expect = 0.0
 Identities = 818/870 (94%), Positives = 818/870 (94%)

Query: 1	MNHPDYKLNLRXXXIFETYMSKEDVS	60
	MNHPDYKLNLR D IFETYMSKEDVS	
Sbjct: 1	MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS MRGKKKSIFETYMSKEDVS	60
Query: 61	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	120
	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	
Sbjct: 61	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	120
Query: 121	WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN	180
	WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN	
Sbjct: 121	WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN	180
Query: 181	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIILEKK	240
	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIILEKK	
Sbjct: 181	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIILEKK	240
Query: 241	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI	300
	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI	
Sbjct: 241	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI	300
Query: 301	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT	360
	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT	
Sbjct: 301	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT	360
Query: 361	IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFVPEGSS	420
	IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFVPEGSS	
Sbjct: 361	IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFVPEGSS	420
Query: 421	LDKVAAERATSVYLVQKVVPMLPRLLCCELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG	480

LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEGKILEEWFG
Sbjct: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEGKILEEWFG 480

Query: 481 RTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQ 540
RTIIRSCTKLSYDHAQSMIEN HSVEEVHQAVLNLHSIAKQLRRQ
Sbjct: 481 RTIIRSCTKLSYDHAQSMIENPTEKIPEEELPPISPEHSVEEVHQAVLNLHSIAKQLRRQ 540

Query: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600
RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP
Sbjct: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT 660
EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT
Sbjct: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720
NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS
Sbjct: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQAF 780
EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQAF
Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQAF 780

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840
DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDV
Sbjct: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840

Query: 841 VLQAEATAALKYSAILKRPGLEKASDEEPED 870
VLQAEATAALKYSAILKRPGLEKASDEEPED
Sbjct: 841 VLQAEATAALKYSAILKRPGLEKASDEEPED 870

>gi|26327097|dbj|BAC27292.1| unnamed protein product [Mus musculus]
Length = 831

Score = 1605 bits (4155), Expect = 0.0
Identities = 801/831 (96%), Positives = 801/831 (96%), Gaps = 14/831 (1%)

Query: 54 MSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV 113
MSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV
Sbjct: 1 MSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV 60

Query: 114 KLLPEDQWK-----AVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS 159
KLLPEDQWK AVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS
Sbjct: 61 KLLPEDQWKPRITLSLPGVLGLQAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS 120

Query: 160 GPDVIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT 219
GPDVIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT
Sbjct: 121 GPDVIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT 180

Query: 220 RGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 279
RGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP
Sbjct: 181 RGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 240

Query: 280 LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339
LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG
Sbjct: 241 LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 300

Query: 340 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD 399
VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD
Sbjct: 301 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD 360

Query: 400 GTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 459
GTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK
Sbjct: 361 GTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 420

Query: 460 LTFSVIWKLTPGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXHS 519
LTFSVIWKLTPGKILEEWFGRTIIRSCTKLSYDHAQSMIEN HS
Sbjct: 421 LTFSVIWKLTPGKILEEWFGRTIIRSCTKLSYDHAQSMIENPTEKIPEEELPPISPEHS 480

Query: 520 VEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579
VEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL
Sbjct: 481 VEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 540

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN 639
VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN
Sbjct: 541 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN 600

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 699
KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS
Sbjct: 601 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 660

Query: 700 PIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 759
PIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL
Sbjct: 661 PIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 720

Query: 760 VKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE 819
VKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE
Sbjct: 721 VKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE 780

Query: 820 PDDLEEEPTQQVITIFSLVDVVLQAEATAALKYSAILKRPGLEKASDEEPED 870
PDDLEEEPTQQVITIFSLVDVVLQAEATAALKYSAILKRPGLEKASDEEPED
Sbjct: 781 PDDLEEEPTQQVITIFSLVDVVLQAEATAALKYSAILKRPGLEKASDEEPED 831

>gi|25047588|ref|XP_129937.2| hypothetical protein MGC37640 [Mus musculus]
Length = 819

Score = 1453 bits (3762), Expect = 0.0
Identities = 720/772 (93%), Positives = 720/772 (93%)

Query: 1 MNHPDYKLNLRXXIFETYMSKEDVS 60
MNHPDYKLNLR D IFETYMSKEDVS
Sbjct: 1 MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS MRGKKKSIFETYMSKEDVS 60

Query: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ
Sbjct: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQOSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180
WKAVKPESNDKEIEATYEADIPEEGCGHHPLQOSRKGWSGPDVIIIEAQFDDSDSEDRHGN
Sbjct: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQOSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240
TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK
Sbjct: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240

Query: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI 300
HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI
Sbjct: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI 300

Query: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360
CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT
Sbjct: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360

Query: 361 IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420
IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS
Sbjct: 361 IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420

Query: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG 480
LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG
Sbjct: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG 480

Query: 481 RTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLAKQLRRQ 540
RTIIRSCTKLSYDHAQSMIEN HSVVEEVHQAVLNLHSLAKQLRRQ
Sbjct: 481 RTIIRSCTKLSYDHAQSMIENPTEKIPPEELPPISPESHSVEEVHQAVLNLHSLAKQLRRQ 540

Query: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600
RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP
Sbjct: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT 660
EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT
Sbjct: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720
NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS
Sbjct: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV 772
EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV
Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV 772

>gi|25019857|ref|XP_110318.2| similar to hypothetical protein MGC37640 [Mus musculus]
Length = 663

Score = 1303 bits (3371), Expect = 0.0
Identities = 647/663 (97%), Positives = 647/663 (97%)

Query: 208 MKDENTPIPDTRGLSEKSLQSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFS 267
MKDENTPIPDTRGLSEKSLQSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFS
Sbjct: 1 MKDENTPIPDTRGLSEKSLQSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFS 60

Query: 268 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327
PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI
Sbjct: 61 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 120

Query: 328 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387
EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD
Sbjct: 121 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 180

Query: 388 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMLPRLLC 447
LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMLPRLLC
Sbjct: 181 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMLPRLLC 240

Query: 448 EELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXX 507
EELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIEN
Sbjct: 241 EELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENPTEKIP 300

Query: 508 XXXXXXXXXXXXHSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567
HSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG
Sbjct: 301 EEELPPISPESHSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 360

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 627
CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG
Sbjct: 361 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 420

Query: 628 LPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY 687
LPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY
Sbjct: 421 LPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY 480

Query: 688 ALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV 747
ALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV
Sbjct: 481 ALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV 540

Query: 748 QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK 807

QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK
 Sbjct: 541 QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK 600

Query: 808 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE 867
 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE
 Sbjct: 601 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE 660

Query: 868 PED 870
 PED
 Sbjct: 661 PED 663

>gi|26325590|dbj|BAC26549.1| unnamed protein product [Mus musculus]
 Length = 684

Score = 1166 bits (3016), Expect = 0.0
 Identities = 569/590 (96%), Positives = 570/590 (96%)

Query: 150 PLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 209
 P +RKGWSGPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK
 Sbjct: 14 PCSSARKGWSGPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 73

Query: 210 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS 269
 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS
 Sbjct: 74 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS 133

Query: 270 DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 329
 DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP
 Sbjct: 134 DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 193

Query: 330 ETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD 389
 ETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD
 Sbjct: 194 ETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD 253

Query: 390 DALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE 449
 DALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE
 Sbjct: 254 DALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE 313

Query: 450 LCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXX 509
 LCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIEN
 Sbjct: 314 LCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENPTEKIPEE 373

Query: 510 XXXXXXXXHSVEEVHQAVLNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCH 569
 HSVEEVHQAVLNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCH
 Sbjct: 374 ELPPISPEHSVEEVHQAVLNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCH 433

Query: 570 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLP 629
 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLP
 Sbjct: 434 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLP 493

Query: 630 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQFRHYAL 689
 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQFRHYAL
 Sbjct: 494 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQFRHYAL 553

Query: 690 NVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCND 739
 NVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCND
 Sbjct: 554 NVPLYTHFTSPIRRFADVIVHRLLAAGLYSEQPDVEPDTLQKQADHCND 603

>gi|23271317|gb|AAH36113.1| Unknown (protein for MGC:33943) [Homo sapiens]
 Length = 612

Score = 916 bits (2368), Expect = 0.0
 Identities = 451/532 (84%), Positives = 476/532 (89%), Gaps = 2/532 (0%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 108
 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG

Sbjct: 42 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 101

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQRKGWS-GPDVIEA 167
DLVVVKLLPE+ WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EA

Sbjct: 102 DLVVVKLLPEEHKVVVKPESNDKETEAAYESDIPEELCGHHPLQQSLKSYNDSPDVIVEA 161

Query: 168 QFDDSDSEDRHGNTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKS 226
QFD SDED HG T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKS

Sbjct: 162 QFDGSDSEDGHGITQNVLVVDGVKKLSVCVSEKGREDDAPVTKDETTTCISQDTRALSEKS 221

Query: 227 LQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQD 286
LQ+SAKVVYILEKKHSRAATG LKLLADKNS+LF+KYALFSPSDHRVPRIYVPLKDCPQD

Sbjct: 222 LQSAKVVYILEKKHSRAATGFLKLLADKNSLFRKYALFSPSDHRVPRIYVPLKDCPQD 281

Query: 287 FMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 346
F+ RPKD+ANTLFICRI+DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS

Sbjct: 282 FVARPKDYANTLFICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 341

Query: 347 SEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGV 406
SEVLECLPQ LPWTIPP+E KRRDLRKDCIFTIDPSTARDLDDAL+C+ L DG F+VGV

Sbjct: 342 SEVLECLPQGLPWTIPPEEFSKRRDLRKDCIFTIDPSTARDLDDALSCKPLADGNFKVGV 401

Query: 407 HIADVSFVPEGSSLDKVAAERATSVYLVQKVPMLPRLLCEELCSLNPMTDKLTFSVIW 466
HIADVSFVPEGS LDKVAAERATSVYLVQKVPMLPRLLCEELCSLNPMTDKLTFSVIW

Sbjct: 402 HIADVSFVPEGSDLDKVAAERATSVYLVQKVPMLPRLLCEELCSLNPMSDKLTFSVIW 461

Query: 467 KLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQA 526
LTPEGKIL+EWFGRTIIRSCTKLSY+HAQSMIE+ HS EEVHQA

Sbjct: 462 TLTPEGKILDEWFGRTIIRSCTKLSYDHAQSMIESPTEKIPAKELPPISPEHSSEEVHQA 521

Query: 527 VLNLHSAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNK 578
VLNLH IAKQLR+QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYR+SNK

Sbjct: 522 VLNLHGIKQLRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRESNK 573

>gi|21753324|dbj|BAC04324.1| unnamed protein product [Homo sapiens]
Length = 603

Score = 812 bits (2098), Expect = 0.0
Identities = 410/527 (77%), Positives = 436/527 (82%), Gaps = 2/527 (0%)

Query: 1 MNHPDYKLNLRXXXIFETYMSKEDVS 60
M+HPDY++NLR D IFETYMSKEDVS

Sbjct: 1 MSHPDYRMNLRPLGTPRGVSAVAGPHDIGASPGDKKSKNRSTRGKKKSIFETYMSKEDVS 60

Query: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPE+

Sbjct: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEEH 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQRKGWS-GPDVIEAQFDDSDSEDRHG 179
WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EAQFD SDED HG

Sbjct: 121 WKVVKPESNDKETEAAYESDIPEELCGHHPLQQSLKSYNDSPDVIVEAQFDGSDSEDGHG 180

Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVYILE 238
T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKSLQ+SAKVVYILE

Sbjct: 181 ITQNVLVVDGVKKLSVCVSEKGREDDAPVTKDETTTCISQDTRALSEKSLQSAKVVYILE 240

Query: 239 KKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTL 298
KKHSRAATG LKLLADKNS+LF+KYALFSPSDHRVPRIYVPLKDCPQDF+ RPKD+ANTL

Sbjct: 241 KKHSRAATGFLKLLADKNSLFRKYALFSPSDHRVPRIYVPLKDCPQDFVARPKDYANTL 300

Query: 299 FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLP 358
FICRI+DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQ LP

Sbjct: 301 FICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQGLP 360

Query: 359 WTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSFVPEG 418

WTIPP+E KRRDLRKDCIFTIDPSTARDLDDAL+C+ L DG F+VGVHIADVSYFVPEG
Sbjct: 361 WTIPPEEFKRRDLRKDCIFTIDPSTARDLDDALSCKPLADGNFKVGVHIADVSYFVPEG 420

Query: 419 SSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEW 478
S LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM+DKLTFSVIW LTPEGKIL+EW
Sbjct: 421 SLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMDSKLTFSVIWTLTPEGKILDEW 480

Query: 479 FGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQ 525
FGRTIIRSCTKLSY+HAQSMIE+ HS EEVHQ
Sbjct: 481 FGRTIIRSCTKLSYHAQSMIESPTEKIPAKELPPISPEHSSEEVHQ 527

>gi|21292324|gb|EAA04469.1| agCP3212 [Anopheles gambiae str. PEST]
Length = 794

Score = 424 bits (1089), Expect = e-117
Identities = 249/672 (37%), Positives = 379/672 (56%), Gaps = 35/672 (5%)

Query: 196 PDRGKEDSSTPVMKDENTPIPOD--TRGLSEKSLQKSAK-VVYILEKKHSRAATGILKLL 252
P +DS+T + N ++ T+ KS Q S VV ILEK+H+R G K L
Sbjct: 127 PKAPSDDSATSPNANGNDESAEEDATQQAGGKSTQNSVGFVVAILEKRHNRCQVG--KFL 184

Query: 253 ADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFM-----TRP 291
A K Y +F P D R+P + V +D P + T
Sbjct: 185 AAAPGK--KHYRVFMPRDMRIPPVRVFKQDWPALLSTNIAKLKDDKEEKEDRKVPQTGD 242

Query: 292 KDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLE 351
D + L+ II+W+++ +G + KS+G+ G +E E E IL E+ +D + + +L
Sbjct: 243 VDVTDLVLYQAEIIEWQDEV--PIGTILKSIGKCGVLEVENESILVEHNLDVTPYGEAILA 300

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411
LP ++P+ IP +E+ +R DLR +CIFTIDP+TARDLDDAL+C++L +G +++GVHI+DV
Sbjct: 301 QLP-AVPYCIPQEELERREDLRGECIFTIDPATARDLDDALSCKQLENGNYQIGVHISDV 359

Query: 412 SYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPE 471
+YF+ E S LD++ RATS+Y+V V MLP+ LC CSL P DKL FSV W++ P+
Sbjct: 360 TYFLRESSPLDELVKLRATSIYMVDTVYHMLPKQLCNT-CSLLPGEDKLAFSVFWEMQPD 418

Query: 472 GKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLH 531
G +L F RT+I SC++LSY+HAQ M++N ++ +++ + V L
Sbjct: 419 GTVLSTRFARTVINSQSLSYHAQLMLDNPSCEVEEDQFPEIMHGYNALQCKIVNTLQ 478

Query: 532 SIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAV 591
SIA QLR++R DG L+++Q KL F LD TG P +Y+ R SN+++E+FMLLAN +V
Sbjct: 479 SIAVQLRQRMDGCLKINQPKLTFRDPATGRPIEYGVYKVRPSNEMIEDFMLLANTSV 538

Query: 592 AHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKY 651
A+ I++ FPE +LLR H PP M+ +LV G + +S + + + +
Sbjct: 539 ANAIYKAFPEISLLRAHSPPAENMMKNLVRTLSLHGHALSYASPKDIRECMETIITSEN 598

Query: 652 SLARKEVLTNMYSRPMQMALYFCGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHR 711
A + VL+ + ++PM A Y+CS E F HYAL +P+YTHFTSPIRR+AD +VHR
Sbjct: 599 PDATRSVLSVLLAKPMIRAQYYCSLYATTPEHFMHYALAIPMYTHFTSPIRRYADCLVHR 658

Query: 712 LLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAM 771
+LAAAL QP P+ LQ A CN+++ +K E S L+F ++ G E+EA
Sbjct: 659 VLAAALVIDVQPKRSPEELQCLAMICNEKKYNACAGEASSLLYFRHWLEAVGEYETEAA 718

Query: 772 VMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQV 831
VMG +++++ G+ + L+ + K +P + + P+D P +
Sbjct: 719 VMGYAAHHIELVLIHSGIVLKAATKKLSTVATVVYK-PTEPVASCMLIPNDTSIPPVE-- 775

Query: 832 ITIFSLVDVVLQ 843
+TIF+ V V ++
Sbjct: 776 LTIFTKVRVTVK 787

>gi|19115422|ref|NP_594510.1| ribonuclease II RNB family protein; dis3-like
[Schizosaccharomyces
pombe]
gi|7493295|pir|T38518 ribonuclease II RNB family protein - fission yeast
(Schizosaccharomyces pombe)
gi|2414618|emb|CAB16367.1| ribonuclease II RNB family protein; dis3-like
[Schizosaccharomyces
pombe]
Length = 927

Score = 418 bits (1075), Expect = e-115
Identities = 273/764 (35%), Positives = 392/764 (51%), Gaps = 91/764 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
++ Y V +GLK GTL +G LRI H + + D ++DG +ARNRA +
Sbjct: 175 VYPLYYDSATVKKGLKSGTLFKGTLRILEN--HRSAFACMEDIPDFYVDGPIARNRAFH 232

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168
D+V+V E D P E LQ + + +
Sbjct: 233 DVVIV-----EPVMNNDSPTEKSNF--LQNG-----VEKVK 261

Query: 169 FDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQ 228
D D E G ++ +++L I + K DS T
Sbjct: 262 IKDHDDE-----LGGAMEHLERLEIKSVASFKGDSRT----- 293

Query: 229 KSAKVYILEKKHSRAATGILKL--LADKNSDLFKK---YALFSPSDHRVPRIYVPLKDC 283
A+VV I ++ GIL+ + KN + K YA+F P D R+P I + D
Sbjct: 294 -RARVVAIEKRAEISKIVGILRAPGWSLKNVEYVSKKSSYAIFIPKDKRLPFITIHKN 352

Query: 284 P----QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339
++++ + LF I W + +G L + LG ++E T +L E G
Sbjct: 353 SDLSGENWIENILKHHDQLFSVEITRWSIYSRYPMGVLGEKLGNIITDVEAYTNALL 412

Query: 340 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD 399
+ S FS EVL CLP W I +E+ KRRDLR + I TIDP TARDLDDA++CR L +
Sbjct: 413 ISSSPFSDEVLNCLPPD-DWIIISHEEIKRRDLRNELIITIDPETARDLDDAVSCR 471

Query: 400 GTFEVGVIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 459
GT+EVGVIADV++FV S+LDK AA RAT+VYLVQK +PMLP LLCE LCSLNP ++
Sbjct: 472 GTYEVGVIADVTHFVKPDSALDKAASRATTVYLVQKAIPMLPPLLCERLCSLNP 531

Query: 460 LTFSVIWKLTPEGK-ILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXX 518
L FSV WKL GK I + WFG+T+I++C +L+Y AQ +IE H
Sbjct: 532 LAFSVFWKLDSNGKEIGRWFGKTVIKTCARLAYSEAQGVIEG--KSWDDAVGKPIGG 589

Query: 519 SVEEVHQAVLNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDS 578
+ ++V ++L L I+++LR+ RF GA+ ++ +L F LD E G+P C +YE D+N
Sbjct: 590 TPKDVETSILTLCESIRKLRKDRFAKGAVEINSTELKFQLD-EYGM PNKCEVYEQT 648

Query: 579 LVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMGLPMDVSSAGAL 638
L+EEFMLLAN +VA I + F +LLRRH P+ K +++ F M D SS+ A
Sbjct: 649 LIEEFMLLANRSVAEHISKNFNSNLSLLRRHASPKEKQINEFCHFLKSMNFD 708

Query: 639 NKSLTK---TFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLY 695
N S+ + TF ++ E+ NM R + A YFC+G ++ + HYAL+ YT
Sbjct: 709 NASMVRLRSTFNEELV-----ELFENMAVRSLNRAEYFCTGDFGEKTDWHHY 763

Query: 696 HFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSGLF 755
HFTSPIRR+ D+IVHRL +L + P ++ A HCN+++ S VQE S LF
Sbjct: 764 HFTSPIRRYPDIIVHRLRLSLK-NTSPGIDKKNCSLVAAHKNEKKEKSTTVQED 822

Query: 756 FAVLVKE-----SGPLESEAMVMGVNLQAFDVLVLRFGVQKRI 793
+V + E + +A + + DV + +G+ R+
Sbjct: 823 LSVYIAEYCKKHDKKSMPVQAFATRISGNSIDVYISEYGISNRV 866

>gi|15220899|ref|NP_177891.1| putative 3'-5' exoribonuclease; protein id:
Atlg77680.1

[Arabidopsis thaliana]
Length = 1055

Score = 414 bits (1063), Expect = e-114
Identities = 277/810 (34%), Positives = 415/810 (51%), Gaps = 78/810 (9%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHNRNEAYCKIDGVPTDILINGNVCQSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168
D VV+KL P W +K E+ EG P + +K + +
Sbjct: 207 DTVVIKLDPLSLWPKMK-----GFVTESAAPKEGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSEDRHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSL 227
F+D S+++ +S + G K ++ S+P + + N G+
Sbjct: 259 FEDGFSKNK---SSVIGKGAKNGVTPSSPPSLDCLGSFCEQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVYILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271
K + +VV ++EK R + G+L + + K SD + +Y P+D
Sbjct: 316 HKRPTGQVVAVVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPDQFMTRPK----DFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327
R P++ VP P R + + L +I+DW E F + Q+ G+ E+
Sbjct: 376 RFPKLIVPFHVLPGSIRARLENLDPNLEAELVAAQIVDWGEGSPFPVAQITHLFGRGSEL 435

Query: 328 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387
EP+ IL + V SDFS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D
Sbjct: 436 EPQINAILYQNSVCDSDFSPLSLTSLPR-VPWEVPEEEVQRRKDLRDLCLVLTIDPSTATD 494

Query: 388 LDDALACRRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMPLRLLC 447
LDDAL+ + L G F VGVHIADVSYFV ++LD A R+TSVYL+Q+ + MLP LL
Sbjct: 495 LDDALSVQSLPGGFVRGVHIADVSYFVLPETALDTEARFRSTSVYLMQRKISMLPPLLS 554

Query: 448 EELCSLNPMTDKLTFSVIWKLTPGKILEWFGRTIIRSC TKLSYDHAQSMIENXXXXXX 507
E + SL+P D+L FS++W L EG +++ W GRTIIRSC KLSYDHAQ +I+
Sbjct: 555 ENVGSLSPGADRLAFSILWDLNREGDVIDRWIGRTIIRSCCKLSYDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKRFRNGALQLENSKPVFLFD-EHGVYPD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 627
+ SN LVEEFMLLANM A I + + +LLRRHP P T+ L + FC + G
Sbjct: 673 FVTCSRKGSNFLVEEFMLLANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKS LTKTFGDDKYS LARKEVLTNMYSRPMQMALYFCSGMLQDQ-EQFRH 686
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H
Sbjct: 733 MDLDISSGQLQDSLEKITGNLKDSDSVFVDILNNYAIKPMQLASYFCTGNLKDVAEWGH 792

Query: 687 YALNVPLYTHFTSPIRRFADVIVHR----LLAAALGYSEQPDVEPD----- 728
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRALAAALEABEELYSKQKQTAIDEGRSCFTGIHFNKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESG 764
L A +CN+R++A+++V++ L+ ++K+
Sbjct: 853 AAESIEGKEALSVAALKHGV PSTEILSDVAAYCNERKLAARKVRDACDKLYTWFVLKQKE 912

Query: 765 PLESEAMVMGVNLQAFDVLVLRFGVQKRIY 794
EA VM + ++ V + + G+++RIY
Sbjct: 913 IFPCEARVMNLGSRFMTVYISKLGIERRIY 942

>gi|25406521|pir||E96806 hypothetical protein T32E8.1 [imported] -
Arabidopsis thaliana
gi|12323300|gb|AAG51632.1|AC012193_14 putative 3'-5' exoribonuclease, 3'
partial; 3320-1 [Arabidopsis
thaliana]
Length = 935

Score = 402 bits (1033), Expect = e-110
Identities = 274/792 (34%), Positives = 404/792 (51%), Gaps = 80/792 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNG 108
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHNRNEAYCKIDGVPTDILINGNVCQSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168
D VV+KL P W +K E+ EG P + +K + +
Sbjct: 207 DTVVIKLDPLSLWPKMK-----GFVTESAAPKEGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSEDRHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSL 227
F+D S+++ +S + G K ++ S+P + + N G+
Sbjct: 259 FEDGFSKNK---SSVIGKGAKNGVTPSSPPSLDSCLSGFCQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVYILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271
K + +VV ++EK R + G+L + + K SD + +Y P+D
Sbjct: 316 HKRPTGQVAVVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPQDFMTRPK---DFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327
R P++ VP P R + + L +I+DW E F + Q+ G+ E+
Sbjct: 376 RFPKLIVPFHVLPGSIRARLENLDPNLEAELVAAQIVDWGEGSPFPVAQITHLFGRGSEL 435

Query: 328 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387
EP+ IL + V SDFS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D
Sbjct: 436 EPQINAILYQNSVCDSDFSPGSLTSLPR-VPWEVPEEEVQRRKDLRDLCLVLTIDPSTATD 494

Query: 388 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 447
LDDAL+ + L G F VGVHIADVSYFV ++LD A R+TSVYL+Q+ + MLP LL
Sbjct: 495 LDDALSVQSLPGGFFRVGVHIADVSYFVLPETALDTEARFRSTSVYLMQRKISMLPPLLS 554

Query: 448 EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXX 507
E + SL+P D+L FS++W L EG +++ W GRTIIRSC KLSYDHAQ +I+
Sbjct: 555 ENVGSLSPGADRLAFSILWDLNREGDVIDRWIGRTIIRSCCKLSYDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFDVGALRLDQLKLAFTLDHETGLPQG 567
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKRFRNGALQLENSKPVFLFD-EHGVFPYD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCDQMG 627
+ SN LVEEFMLLANM A I + + +LLRRHP P T+ L + FC + G
Sbjct: 673 FVTCSRKGSNFLVEEFMLLANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKS LTKTFGDDKYS LARKEVLTNMYSRPMQMALYFCSGMLQDQ-EQFRH 686
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H
Sbjct: 733 MDLDISSGQLQDSLEKITGNLKDSDSVFVDILNNYA IKPMQLASYFCTGNLKD SVAEWGH 792

Query: 687 YALNVPLYTHFTSPIRRFADVIVHR----LLAAALGYSEQPDVEPD----- 728
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRALAAALEAEELYSKQKQTAIDEGRSCFTGIHFNKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLF--FAVLVKE 762
L A +CN+R++A+++V++ L+ F + KE
Sbjct: 853 AAESIEGKEALSVAALKHGV PSTEILSDVAAYCNERKLAARKVRDACDKLYTWFLVKQKE 912

Query: 763 SGPLESEAMVMG 774
P E+ M +G
Sbjct: 913 IFPCEARVMNLG 924

>gi|25332397|pir||A84553 probable mitotic control protein dis3 [imported] -
Arabidopsis

thaliana
Length = 955

Score = 396 bits (1018), Expect = e-109
Identities = 252/757 (33%), Positives = 407/757 (53%), Gaps = 84/757 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRIIDGVVARNRALNG 108
I++ + +++ GL RG QG LR+N +EA++ S +I I G NRA +G
Sbjct: 215 IYQEHKPMSEITAGLHRGIYHQKLRVNRFPYEAAYVGSESIGEEIIYGRSNMNRADF 274

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168
D+V V+LLP DQW+ ++K + EA I S DV++
Sbjct: 275 DIVAVELLPRDQWQ-----DEKALSIAEEAVI-----SLHDVVVLNLS 311

Query: 169 F---DDSDSEDRHGNTSGL---VDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRG 221
F +S+++D +T L VD + S + + + ++ PV
Sbjct: 312 FFQISNSNADDEEDDTVHLAPDNVDDAPRTSNLSHETSGDKNAAPV----- 357

Query: 222 LSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281
+ S +VV ++ +++ + G L+ ++ +ALF D R+P+I + +
Sbjct: 358 -----RPSGRVVGVI-RRNWHSYCGSLEPMSLPAGSGGTAHALFVSKDRRIPKIRINTR 410

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVD 341
++ + + + W + G + +G+ G+ E ETE +L E VD
Sbjct: 411 QL-----QNLDMRIVVAVDSWDRQSRYPGSHYVRPIGKIGDKETETEVVLIENDVD 462

Query: 342 FSDFSSEVLECLPQSLPWTIPPDEVGK--RRDLRKDCIFTIDPSTARDLDDALACRRLTD 399
+S FSS+VL CLP LPW++ ++V R+DLR +F++DP +D+DDAL C L +
Sbjct: 463 YSPFSSQVLACLP-PLPWSVSSDVSNPVRQDLRHLLVFSVDPPGCKDIDDALHCTSLPN 521

Query: 400 GTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMPTDK 459
G FE+GVHIADV+ FV G+ LD A++R TSVYLV++ + MLP+ L E++CSL ++
Sbjct: 522 GNFEVGVIADVTFNVHPTPLDDEASKRGTSVYLVERRIDMLPKPLTEDICSLRADVER 581

Query: 460 LTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHS 519
L FSVIW+++P+ +I+ F ++II+S LSY AQ+ +++
Sbjct: 582 LAFSVIWEMSPDAEIISTRFTKSIKSSAALSYIEAQARMDDSR----- 626

Query: 520 VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579
+ + + N++++AK +R++R GAL L ++ F +D E P +Y+ ++N++
Sbjct: 627 TDSLTTDLRNMNTLAKIMRQRRIDRGALTASAEVKFDIDPENHDPLNIGMYQILEANQM 686

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMGLPMDVSSAGALN 639
VEEFML AN++VA +I + FP +LLRRHP P +ML L+ +GL +DVSS+ AL
Sbjct: 687 VEEFMLAANVSVAGQILKLFPSCSLLRRHPTPTREMLEPLLRATAAIGLTLDVSSSKALA 746

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 699
SL + G+D Y +++ + +R M A+YFCSG L E + HY L PLYTHFTS
Sbjct: 747 DSLDRAVGEDPYF---NKLIRILATRCMTQAVYFCSGDLSPPE-YHHYGLAAPLYTHFTS 802

Query: 700 PIRRFADVIVHRLLAALGYSEQPDVEPD--TLQKQADHCNDRMASKRVQELSIGLFFA 757
PIRR+ADV VHRLLAAL+LG + P V D L AD+ N R ++ S+ L+
Sbjct: 803 PIRRYADVIVHRLLAASLGIYKLPTVFQDRPQLTSVADNLNRYHRNAQMAGRASVELYVL 862

Query: 758 VLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIY 794
+ + + P + EA V+ + + F V V ++G++ +Y
Sbjct: 863 IYFR-TRPTDEEARVVKIRSNGFIVFVPKYGIEGPVY 898

>gi|24654592|ref|NP_728490.1| CG16940-PC [Drosophila melanogaster]
gi|23092667|gb|AAN11425.1|AE003467_37 CG16940-PC [Drosophila melanogaster]
Length = 1044

Score = 367 bits (942), Expect = e-100
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGV---VARNRALNGDLVVVKLL-PEDQ 120
G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q
Sbjct: 308 GRIVVEEIRVNRKNNRQAFIIMSTDREALERDGI VLLPVARRYAFDGDKVRAFVLNPGAQ 367

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180
+ E + EI G P G E DD++S+ +
Sbjct: 368 GSSKTAEPSSGEIS-----GGKPSLSLADG-----EELSDDTESQGSSED 407

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240
T +V V+ +N P A V+ I ++
Sbjct: 408 TDNVV-----VISSDNCP-----KAFVIAITKRT 431

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPK-D 293
R G + KL D+ LF K F P D RVP +YVP C + + D
Sbjct: 432 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPMVYVPKDACAAHIGNKQQID 485

Query: 294 FANTLFICRIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351
+ L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++
Sbjct: 486 VSGLLYLAHILE--TDCNGHCIAELIQPVGRVGNLDELKAILFHNGLRDIKPFQRFID 543

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRRLTDGTFEVGVHIADV 411
Q P I +++ +R+DLRK CIFTIDP TARDLDDA++ +L D +E+GVHI+DV
Sbjct: 544 IYSQPPP-PISQEDLRQRKDLRKMCIFTIDPMTARDLDDAVSIEKLG DNEYEIGVHISDV 602

Query: 412 SYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPE 471
S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +
Sbjct: 603 SHFLIEDNELDNIVKERSTSIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 661

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529
G +L++ F RT+I SC++ +Y+HAQ +I+N + +++ VL
Sbjct: 662 GVMLQKKPEFCRTVINSCSQFAYEHAQKIIDNPNERFTENDFPTILNGFNPDDIRNRVLW 721

Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMLLAN
Sbjct: 722 LHDIASSIRKTRLDNGALTINNAKLRFLLDPTIGEPLSFEVEKQREANRLIEEFMLLANQ 781

Query: 590 AVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDQGLPMDVSSAGALNKSLTKTFGDD 649
AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +
Sbjct: 782 AVARFIHDSFPDIAVLRNHPPLIKSLKALREKLLALGFELDYSSSKALQESMVRLCNEA 841

Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIV 709
+A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V
Sbjct: 842 PNPVAMNACLSQLLMKPMARATYFCSEKSEPADLWHYALSIPIYTHFTSPIRRYPDILV 901

Query: 710 HRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE 769
HRLLAAL Y P PD L N+R+ +K+ E S L+F V +
Sbjct: 902 HRLLAALKYCTPPKRTPDLDLHTLTKLANERKYNKAGEDSGNLYFKRYVHNKQGIYMR 961

Query: 770 AMVMGVNLQAFDVLVLRFG 788
A+V+ + +V+ L G
Sbjct: 962 AVVIEIFQHMMNVVTLESG 980

>gi|19922976|ref|NP_612012.1| CG16940-PA [Drosophila melanogaster]
gi|24654597|ref|NP_728491.1| CG16940-PB [Drosophila melanogaster]
gi|16198179|gb|AAL13898.1| LD37985p [Drosophila melanogaster]
gi|23092668|gb|AAF47351.2| CG16940-PA [Drosophila melanogaster]
gi|23092669|gb|AAN11426.1|AE003467_39 CG16940-PB [Drosophila melanogaster]
Length = 1032

Score = 367 bits (942), Expect = e-100
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGV---VARNRALNGDLVVVKLL-PEDQ 120
 G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q
 Sbjct: 296 GRIVEEEIRVNRKNNRQAFIIMSTDREALERDGIIVLLPVARRYAFDGDKVRAFVLNPGAQ 355

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQRKGWSGPDVIEAQFDDSDSEDRHGN 180
 + E + EI G P G E DD++S+ +
 Sbjct: 356 GSSKTAEPSSGEIS-----GGKPSLSLADG-----EELSDDTESQGSESD 395

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240
 T +V V+ +N P A V+ I ++
 Sbjct: 396 TDNVV-----VISSDNCP-----KAFVIAITKRT 419

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPK-D 293
 R G + KL D+ LF K F P D RVP +YVP C + + D
 Sbjct: 420 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPMVYVPKDACAHAHGNKQQID 473

Query: 294 FANTLFICRIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351
 + L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++
 Sbjct: 474 VSGLLYLAHILE--TDCNGHCIAELIQPVGRVGNLDELKAILFHNGLRDIKPFEQRFID 531

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411
 Q P I +++ +R+DLRK CIFTIDP TARDLDDA++ +L D +E+GVHI+DV
 Sbjct: 532 IYSQPPP-PISQEDLRQRKDLRKMCIFTIDPMTARDLDDAVSIEKLG DNEYEIGVHISDV 590

Query: 412 SYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCSEELCSLNPMTDKLTFSVIWKLTP 471
 S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +
 Sbjct: 591 SHFLIEDNELDNIVKERSTSIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 649

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529
 G +L++ F RT+I SC++ +Y+HAQ +I+N + +++ VL
 Sbjct: 650 GVMLQKKPEFCRTVINSCSQFAYEHAQKIIDNPNERNFTENDFPTILNGFNPD DIRNRVLW 709

Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
 LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMLLAN
 Sbjct: 710 LHDIASSIRKTRLDNGALTINNAKLRFLLD PITGEPLSFEVEKQREANRLIEEFMLLANQ 769

Query: 590 AVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDQMG LPM DVSSAGALNKSLTKTFGDD 649
 AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +
 Sbjct: 770 AVARFIHDSFPDIAVLRNHPPPLIKSLKALREKLLALGFELDYSSSKALQESMVRLCNEA 829

Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIRRFADVIV 709
 +A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V
 Sbjct: 830 PNPVAMNACLSQLLMKPMARATYFCSE GKSEPADLWHYALSIPYTHFTSPIRRYPDILV 889

Query: 710 HRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE 769
 HRLLAAL Y P PD L N+R+ +K+ E S L+F V +
 Sbjct: 890 HRLLAALKYCTPPKRTPD LHTLTKLANERKYNKAGEDSGNLYFKRYVHNKQGIYMR 949

Query: 770 AMVMGVNLNQA FDLVLRFG 788
 A+V+ + +V+ L G
 Sbjct: 950 AVVIEIFQHMMNVVTLESG 968

>gi|15292611|gb|AAK93574.1| SD10981p [Drosophila melanogaster]
 Length = 982

Score = 351 bits (901), Expect = 2e-95
 Identities = 249/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGD 109
 + ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD
 Sbjct: 232 YPPHLSMKELLEGLRQNKLLQGTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQRKGWSGPDVIEAQF 169
 LV V+LLPE +W A P E + Y ++P
 Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQK 229
SE+R + + +++ V+ ++S E TP
Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 347
N I I W + + G +SLG G++ E E IL E+ V FS
Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRS LGPLGDMATENEVILLEHDVPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVH 407
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPGCTDIDDALHCRELPNGNLEVGVH 512

Query: 408 IADVSFVPEGSSLDKVAAERATSVYLVQKVPMLPRLLCSEELCSLNPMTDKLTFSVIWK 467
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+
Sbjct: 513 IADVSHFIRPGNALDMEAAARGTTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRITIRCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAV 527
+ E +L + F +++I+S ++Y+ AQ++I++ E+ +++
Sbjct: 573 VDNEANVLSKRFHKSIVKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLA 587
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA
Sbjct: 618 RNLNRLAKILKKRRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNMVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTF- 646
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K
Sbjct: 678 NITVAEHIAFESECAVLRHPRPPPTNFDPLVKSARYQGFQVDINSGLELSHSLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQFRHYALNVPLYTHFTSPIRRFAD 706
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D
Sbjct: 738 ADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYS 793

Query: 707 VIVHRLLAALG----YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762
++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +
Sbjct: 794 IMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYHKMAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDD 822
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEED 908

Query: 823 LEEPTQQVITIFSLVDVVLQAEATAALKYSAILKR 857
+ V F V V L +++ +++ ++ R
Sbjct: 909 HTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|18488261|ref|XP_081229.1| Dis3 [Drosophila melanogaster]
gi|24649634|ref|NP_651246.2| CG6413-PA [Drosophila melanogaster]
gi|7301148|gb|AAF56281.1| CG6413-PA [Drosophila melanogaster]
Length = 982

Score = 350 bits (898), Expect = 6e-95
Identities = 248/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGD 109
+ ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD
Sbjct: 232 YPPHLSMKELLEGLRQNKLLQGTTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQF 169
LV V+LLPE +W A P E + Y ++P
Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEV----- 322

Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQK 229
SE+R + + +++ V+ ++S E TP
Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347
N I I W + + G +SLG G++ E E IL E+ V FS
Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRS LGPLGDMATENEVILLEHDVPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVG V 407
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL C+ L +G EVGVH
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPPGCTDIDDALHCKELPNGNLEVG V 512

Query: 408 IADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWK 467
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+
Sbjct: 513 IADVSHFIRPGNALDMEAAARGTTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAV 527
+ E +L + F +++I+S ++Y+ AQ++I++ E+ +++
Sbjct: 573 VDNEANVLSKRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLA 587
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA
Sbjct: 618 RNLNRLAKILKKRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFC DQMGLPMDVSSAGALNKS LTKTF- 646
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K
Sbjct: 678 NITVAEHIAFSECAVLRHPRPPPTNFDPLVKSARYQGFQVDINSGLELSHSLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFAD 706
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D
Sbjct: 738 ADNPFYNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYS D 793

Query: 707 VIVHRLLAALG----YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762
++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +
Sbjct: 794 IMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYHKMAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDD 822
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEED 908

Query: 823 LEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857
+ V F V V L +++ +++ ++ R
Sbjct: 909 HTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|21748526|dbj|BAC03400.1| FLJ00327 protein [Homo sapiens]
Length = 266

Score = 343 bits (879), Expect = 9e-93
Identities = 167/188 (88%), Positives = 175/188 (93%)

Query: 578 KLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFC DQMGLPMDVSSAGA 637
+LVEEFMLLANMAVAHKI R FPEQALLRRHPPPQT+MLSDLVEFC DQMGLP+D SSAGA
Sbjct: 29 RLVEEFMLLANMAVAHKIHRAFPEQALLRRHPPPQTRMLSDLVEFC DQMGLPVDFSSAGA 88

Query: 638 LNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHF 697
LNKSLT+TFGDDKYSLARKEVLTNM SRPMQMALYFCSG+LQD QFRHYALNVPLYTHF
Sbjct: 89 LNKSLTQTFGDDKYSLARKEVLTNMC SRPMQMALYFCSGLLQDPAQFRHYALNVPLYTHF 148

Query: 698 TSPIRRFAADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFA 757
TSPIRRFAADV+VHRLLAALGY E+ D+ PDTLQKQADHCNDRRMASKRVQELS LFFA
Sbjct: 149 TSPIRRFAADVLVHRLLAALGYRERLDMAPDTLQKQADHCNDRRMASKRVQELSTSLFFA 208

Query: 758 VLVKESGP 765
VLVK S P
Sbjct: 209 VLVKVSP 216

>gi|26327903|dbj|BAC27692.1| unnamed protein product [Mus musculus]
Length = 687

Score = 340 bits (871), Expect = 7e-92
Identities = 233/670 (34%), Positives = 344/670 (51%), Gaps = 60/670 (8%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVYILEKKHSRAATGILKL 251
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L
Sbjct: 36 SVVLDDEGQONEDD--VEKDEERELLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 91

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQFMTRPKDFANTLFICRIIDWKEDCN 311
K S + LF+P+D R+PRI + + I I W +
Sbjct: 92 SDIKES----RRHLFTPADKRIPRIRIETR-----QASALEGRRIIVAIDGWPRNSR 139

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRD 371
+ G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D
Sbjct: 140 YPNGHFVKNLGDVGEKETETEVLLLEHDVPHQPFSSQAVLSFLPR-MPWSITEEDMKNRED 198

Query: 372 LRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIAVSVFVPEGSSLDKVAERATS 431
LR C+ ++DP D+DDAL CR L++G EVGVHIAVSV+F+ G++LD+ +A R T+
Sbjct: 199 LRHLCVCSVDPPGCTDIDDALHCRELSNGNLEVGVHIAVSHFIRPGNALDQESARRGTT 258

Query: 432 VYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRITIRSC TKLS 491
VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S L+
Sbjct: 259 VYLCEKRIDMVPELLSSNLCSLRSNVDRLAFSCIWEMNHNAEILKTRFTKSVINSKASLT 318

Query: 492 YDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQ 551
Y AQ I++ +++ ++ L+ +AK L++ R GAL L
Sbjct: 319 YAEAQMRIDSAAMN-----DDITSLRGLNQLAKILKKGRIEKGALTLSS 363

Query: 552 LKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611
++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+HP P
Sbjct: 364 PEIRFHMDSETHDPIDLQTKELRETNSMVEEFMLLANISVAKKIHEEFSEHALLRKHPAP 423

Query: 612 QTKMLSDLVEFCQDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQMAL 671
LV+ L + +A +L SL + D L +L + +R M A+
Sbjct: 424 PPSNYDILVKAASKNLQIKTDTAKSLADSLDRAESPDPYL--NTLLRILATRCMMQAV 481

Query: 672 YFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG----YSEQPDVEP 727
YFCSGM D F HY L P+YTHFTSPIRR+AD+IVHRLLA A+G Y E D
Sbjct: 482 YFCSGMDND---FHHYGLASPIYTHFTSPIRRYADIIVHRLLAIVAIGADCTYPELTDK-- 536

Query: 728 DTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLV 784
K +D C N R ++ Q S+ + K G + EA ++ V A VL+
Sbjct: 537 ---HKLS DICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILFVRKNAIVVLI 593

Query: 785 LRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQA 844
++G++ ++ +K KP L E L E T V +F V V +
Sbjct: 594 PKYGLEGTVFFE-----EKDKPKPRLAYDDEIPSLRIEGT--VFHVFDKVKVKITL 642

Query: 845 EATALKYS AI 854
+++ L++ I
Sbjct: 643 DSSNLQH QKI 652

Score = 37.7 bits (86), Expect = 0.87
Identities = 20/54 (37%), Positives = 32/54 (59%), Gaps = 2/54 (3%)

Query: 91 DRDIFIDGVVARNRALNGDLVVVKKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144
+++I I G+ NRA++ D+V V+LLP QW V P S + E E D+ ++

Sbjct: 1 EKEILIQGIKHLNRAVHEDIVAVELLPRSQW--VAPSSVVLDDDEGQNEDDVEKD 52

>gi|13446610|emb|CAC35051.1| putative exoribonuclease DIS3 [Drosophila melanogaster]
Length = 983

Score = 335 bits (859), Expect = 2e-90
Identities = 244/816 (29%), Positives = 401/816 (49%), Gaps = 111/816 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGD 109
+ ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD

Sbjct: 232 YPPHLSMKELLEGLRQNKLLQGTFAQSRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQF 169
LV V+LLPE +W A P E + Y ++P

Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQK 229
SE+R + + +++ V+ ++S E TP

Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +

Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347
N I I W + + G +SLG G++ E E IL E+ V FS

Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRSGLGPLGDMATENEVILLEHDPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVH 407
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH

Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPPGCTDIDDALHCRELPNGNLEGVH 512

Query: 408 IADVSYFVPEGSSLDKVAARA-TSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIW 466
IADVS+F+ G + T+VYLV K + M+P LL LCSL ++ FS +W

Sbjct: 513 IADVSHFIRPGKRTGHGGSGPGETTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVW 572

Query: 467 KLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQA 526
++ E +L + F +++I+S ++Y+ AQ++I++ E+ ++

Sbjct: 573 EVDNEANVLKSRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKS 617

Query: 527 VLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLL 586
+ NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLL

Sbjct: 618 LRNLNRLAKILKKRRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNMVEEFMLL 677

Query: 587 ANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSILTKTF 646
AN+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K

Sbjct: 678 ANITVAEHIATEFSECAVLRHPRPPPTNFDPLVKSARYQGFQVDINSGLLELSHSLDKCV 737

Query: 647 -GDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFA 705
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++

Sbjct: 738 KADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYS 793

Query: 706 DVIVHRLLAALG----YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVK 761
D++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +

Sbjct: 794 DIMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYRHKMAQYAGRASVALNTHLFFR 851

Query: 762 ESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPD 821
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +

Sbjct: 852 GKEE-DEEGYVLFVRKNALQVLIPIKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEE 908

Query: 822 DLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857
D + V F V V L +++ +++ ++ R

Sbjct: 909 DHTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 944

>gi|5262619|emb|CAB45749.1| hypothetical protein [Homo sapiens]
Length = 632

Score = 334 bits (856), Expect = 4e-90
Identities = 226/644 (35%), Positives = 335/644 (52%), Gaps = 65/644 (10%)

Query: 222 LSEKSLQKSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281
+SEK L+ + +VV I+ K++ R G+L K S + LF+P+D R+PRI + +
Sbjct: 8 VSEKMLKPTGRVVGII-KRNWRPYCGMLSKSDIKES----RRHLFTPADKRIPRIRIETR 62

Query: 282 DCPQDFMTRPKDFANTLFICRII----DWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337
A+TL RII W + + G ++LG GE E ETE +L E
Sbjct: 63 Q-----ASTLEGRRIIVAIDGWPRNSRYPNGHFVRNLGVDVGEKETETEVLLLE 110

Query: 338 YGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRL 397
+ V FS VL LP+ +PW+I ++ R DLR CI ++DP D+DDAL CR L
Sbjct: 111 HDVPHQPFSSQAVLSFLPK-MPWSITEKDMKNREDLRHLCICSVDPGCTDIDDALHCREL 169

Query: 398 TDGTFEVGVIADVSFYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM 457
+G EVGVIADVS+F+ G++LD+ +A R T+VYL +K + M+P LL LCSL
Sbjct: 170 ENGNLEVGVIADVSHFIRPGNALDQESARRGTTVYLCEKRIDMVPELLSSNLCSLKCDV 229

Query: 458 DKLTFSVIWKLTPPEGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXXXXXXX 517
D+L FS IW++ +IL+ F +++I S L+Y AQ I++
Sbjct: 230 DRLAFSCIWEMNHNAEILKTKFTKSVINSKASLTAEALRIDSANMN----- 277

Query: 518 HSVEEVHQAVLNHLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSN 577
+++ ++ L+ +AK L+++R GAL L ++ F +D ET P E R++N
Sbjct: 278 ---DDITSLRGLNKLAKILKKRRIEKGALTLSSPEVRFHMDSETHDPIDLQTKELRETN 334

Query: 578 KLVVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCQDQGLPMDVSSAGA 637
+VEEFMLLAN++VA KI F E ALLR+HP P LV+ L + +A +
Sbjct: 335 SMVEEFMLLANISVAKKIHVEEFSEHALLRKHPAPPPSNYEILVKAARSRNLEIKTDTAKS 394

Query: 638 LNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHF 697
L +SL + L +L + +R M A+YFCSGM D F HY L P+YTHF
Sbjct: 395 LAESLDQAESPTFPYL--NTLLRILATRCMMQAVYFCSGMDND---FHHYGLASPIYTHF 449

Query: 698 TSPIRRFADVIVHRLLAALG----YSEQPDVEPDTLQKQADHC---NDRRMASKRVQEL 750
TSPIRR+ADVIVHRLLA A+G Y E D K AD C N R ++ Q
Sbjct: 450 TSPIRRYADVIVHRLLAVAIGADCTYPELTDK-----HKLADICKNLNFRHKMAQYAQRA 504

Query: 751 SIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVVGK 810
S+ + K G + EA ++ V A VL+ ++G++ + F +
Sbjct: 505 SVAFHTQLFFKSKGIVSEEAYILFVRKNAIVVLIPKYGLEGTV-----FFEEKD 553

Query: 811 KPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAI 854
KP L+++ + + V +F V V + +++ L++ I
Sbjct: 554 KPNPQLIYDDEIPSLKIEDTVFHVFDKVKVKIMLDSSNLQHOKI 597

>gi|27703387|ref|XP_224449.1| similar to mitotic control protein dis3
homolog [Homo sapiens]
[Rattus norvegicus]
Length = 1034

Score = 330 bits (846), Expect = 7e-89
Identities = 233/679 (34%), Positives = 343/679 (50%), Gaps = 69/679 (10%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVYILEKKHSRAATGILKL 251
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L
Sbjct: 374 SVVLHDEGQNEED--VEKDEERELLLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 429

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCN 311
K S + LF+P+D R+PRI + + + I I W +
Sbjct: 430 SDIKES----RRHLFTPADKRIPRIRIETR-----QASALEGRRIIIVADGWPRNSR 477

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRD 371
+ G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D
Sbjct: 478 YPNGHFVKNLGDVGEKETETEVLLLEHDVPHQPFSSQAVLSFLPK-MPWSITEEDMKNRED 536

Query: 372 LRKDCIFTIDPSTARDLDDALACRRITDGTFEVGVHIADVSYFVPEGSSLDKVAAERATS 431
LR C+ ++DP D+DDAL CR L++G EVGVHIADVS+F+ G++LD+ +A R T+
Sbjct: 537 LRHLCVCSVDPPGCTDIDDALHCRELSNGNLEVGVHIADVSHFIRPGNALDQESARRGTT 596

Query: 432 VYLVQKVVPMLPRLLCEELCSLNPMTDKL-----TFSVIWKLTPEGKILEEWFGRT 482
VYL +K + M+P LL LCSL D+ F IW++ +IL+ F ++
Sbjct: 597 VYLCEKRIDMVPELLSSNLCSLRSNVDRYFCIVFDKXWHFPXIWEMNHNAEILKTRFTKS 656

Query: 483 IIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRF 542
+I S L+Y AQ I++ +++ ++ L+ +AK L+R R
Sbjct: 657 VINSKASLTAEQAQMRIDSAAMN-----DDITSLRGLNKLAKILKRGRI 701

Query: 543 VDGA LRDLQKLAFITLDHETGLPQGCHIYEYRDSNKLVEEFMMLLANMAVAHKIFRTFPEQ 602
GAL L ++ F +D ET P E R++N +VEEFMMLLAN++VA KI F E
Sbjct: 702 EKGALTLSSPEIRFHMDSETHDPIDLQTKELRETNSMVEEFMMLLANISVAKKIHEEFSEH 761

Query: 603 ALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSITKTFGDDKYSLARKEVLTNM 662
ALLR+HP P LV+ L + +A +L SL + D L +L +
Sbjct: 762 ALLRKHPAPPPSNEYVLVKAASKNLEIRTD TAKSLADSLDRAECPDFPYL--NTLLRIL 819

Query: 663 YSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG---- 718
+R M A+YFCSGM D F HY L P+YTHFTSPIRR+AD+IVHRLLA A+G
Sbjct: 820 ATRCMMQAVYFCSGMDS--FHHYGLASPIYTHFTSPIRRYADIIVHRLLAIVAIGADCT 876

Query: 719 YSEQPDVEPDITLQKQADHC--NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775
Y E D K +D C N R ++ Q S+ + K G + EA ++ V
Sbjct: 877 YPELTDK-----HKLS DICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILFV 931

Query: 776 LNQA FDLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIF 835
A VL+ ++G++ ++ +K KP LT E L E T V +F
Sbjct: 932 RKN AIVVLIPKYGLEGT VFFE-----EKDKPKPRLTYDDEIPSLRIEGT--VFHV 980

Query: 836 SLVDVVLQAEATAALKYSAI 854
V V + +++ L++ I
Sbjct: 981 DKVKVKITLDSSNLQHOKI 999

Score = 51.6 bits (122), Expect = 5e-05
Identities = 30/99 (30%), Positives = 54/99 (54%), Gaps = 5/99 (5%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFI---PSPDGDRDIFIDGVVARNRA 105
IF ++ + +G+K G+ +QG R + + + EA + + +++I I G+ NRA
Sbjct: 294 IFSEHLPLSKLQQGIKSGSYLQGTFRASRENYLEATVWIHGDKEDKEKEILIQGLKHLNRA 353

Query: 106 LNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144
++ D+V V+LLP+ QW V P S E E D+ ++
Sbjct: 354 IHEDIVAVELLPKSQW--VAPSSVVLHDEGQNEEDDVEKD 390

>gi|19923416|ref|NP_055768.2| mitotic control protein dis3 homolog [Homo sapiens]
gi|17225572|gb|AAL37479.1|AF330044_1 KIAA1008 protein [Homo sapiens]
Length = 958

Score = 330 bits (845), Expect = 7e-89
Identities = 229/674 (33%), Positives = 344/674 (51%), Gaps = 68/674 (10%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIYILEKKHSRAATGILKL 251
S+ D G+ + ++ + +SEK L+ + +VV +I+ K++ R G+L
Sbjct: 307 SVVLHDEGQNEEDVEKEEETERMLKT--AVSEKMLKPTGRVVGII-KRNWRPYCGMLSK 362

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRII----DWK 307
K S + LF+P+D R+PRI + + A+TL RII W
Sbjct: 363 SDIKES----RRHLFTPADKRIPRIRIETRO-----ASTLEGRRRIIVADGWP 406

Query: 308 EDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVG 367
+ + G ++LG GE E ETE +L E+ V FS VL LP+ +PW+I ++
Sbjct: 407 RNSRYPNGHFVRNLGVDGKETETEVLLLEHDVPHQPFSSQAVLSFLPK-MPWSITEKDMK 465

Query: 368 KRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFYFVPEGSSLDKVAEE 427
R DLR CI ++DP D+DDAL CR L +G EVGVHIADVS+F+ G++LD+ +A
Sbjct: 466 NREDLRHLCICSVDPGCTDIDDALHCRELENGNLEVGVIADVSHFIRPGNALDQESAR 525

Query: 428 RATSIVLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRITIRSC 487
R T+VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S
Sbjct: 526 RGTTVYLCEKRIDMVPELLSSNLCSLKCDVDRLAFSCIWEMNHNAEILKTKFTKSVINSK 585

Query: 488 TKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGAL 547
L+Y AQ I++ +++ ++ L+ +AK L+++R GAL
Sbjct: 586 ASLTAEQAQLRIDSANMN-----DDITTSRLGLNKLAKILKKRRIEKGA 630

Query: 548 RLDQLKLAFTLDHETGLPQGCHIYERDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRR 607
L ++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+
Sbjct: 631 TLSSPEVRFHMDSETHDPIDLQTKELRETNSMVEEFMLLANISVAKKIHEEFSEHALLRK 690

Query: 608 HPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPM 667
HP P LV+ L + +A +L +SL + L +L + +R M
Sbjct: 691 HPAPPPSNYEILVKAARSRLNLEIKTDTAKSLAESLDQAESPTFPYL--NTLLRILATRCM 748

Query: 668 QMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG---YSEQP 723
A+YFCSGM D F HY L P+YTHFTSPIRR+ADVIVHRLLA A+G Y E
Sbjct: 749 MQAVYFCSGMDND---FHHYGLASPIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELT 805

Query: 724 DVEPDTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAF 780
D K AD C N R ++ Q S+ + K G + EA ++ V A
Sbjct: 806 DK-----HKLADICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILEFVRKNAI 860

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840
VL+ ++G++ + F + KP L+++ + + V +F V V
Sbjct: 861 VVLIPKYGLEGTV-----FFEEKDKPNPQLIYDDEIPSLKIEDTVFHVFDKVKV 909

Query: 841 VLQAEATAALKYSAI 854
+ +++ L++ I
Sbjct: 910 KIMLDSSNLQHOKI 923

Score = 50.1 bits (118), Expect = 2e-04
Identities = 27/83 (32%), Positives = 48/83 (57%), Gaps = 5/83 (6%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFI---PSPDGDRDIFIDGVVARNRA 105
IF ++ + +G+K GT +QG R + + + EA + + +++I + G+ NRA
Sbjct: 227 IFSEHLPLSKLQQGIKSGTYLQGTFRASRENYLEATVWIHGDSEENKEIILQGLKHLNRA 286

Query: 106 LNGDLVVVKLLPEDQWKAVKPES 128
++ D+V V+LLP+ QW V P S
Sbjct: 287 VHEDIVAVELLPKSQW--VAPSS 307

>gi|6324552|ref|NP_014621.1| Possible component of RCC1-Ran pathway; Dis3p
[Saccharomyces cerevisiae]
gi|2500547|sp|Q08162|RR44_YEAST Exosome complex exonuclease RRP44
(Ribosomal RNA processing protein
44) (Protein DIS3)
gi|2131990|pir||S66704 hypothetical protein YOL021c - yeast (Saccharomyces
cerevisiae)
gi|1419801|emb|CAA99021.1| ORF YOL021c [Saccharomyces cerevisiae]

gi|1754617|dbj|BAA11176.1| DIS3 protein [Saccharomyces cerevisiae]
Length = 1001

Score = 321 bits (823), Expect = 3e-86
Identities = 253/761 (33%), Positives = 364/761 (47%), Gaps = 99/761 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGD 109
F Y S V GLK G L QG ++I+ F E + P + + I G NRA NGD
Sbjct: 255 FPEYYSTARVMGGLKNGVLYQGNIQISEYNFLEGSVSLPRFSKPV LIVGQKNL NRAFNGD 314

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQF 169
V+V+LLP+ +WKA D E H + + PD IEA
Sbjct: 315 QVIVELL PQSEWKAPSSIVLDSE-----HFDVNDN-----PD--IEAG- 350

Query: 170 DDSDEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDQTRGLSEKSLQK 229
DD D+ + NT+ + D ++L + KD I Q + K +Q
Sbjct: 351 DDDDNNESSSNTTVISDKQRR-----LAKD--AMIAQRS-----KKIQP 388

Query: 230 SAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKD-CPQDFM 288
+AKVVYI +++ R G LA + D P ++V L D C
Sbjct: 389 TAKVVYI-QRRSWRQYVG---QLAPSSVD-----PQSSSTQNVFVILMDKCLPKVR 435

Query: 289 TRPKDFANTL---FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDF 345
R + A L + I W + LG + LG + ETE +L E+ V++ F
Sbjct: 436 IRTTAAELLDKRIVISIDSWPTTHKYPLGHFVRDLGTIESAQAEATEALLLEHDVEYRPF 495

Query: 346 SSEVLECLP-QSLPWTIP-----PDEVG-----KRRDLRKDCIFTIDPSTARDLDDALA 393
S +VLECLP + W P P+ V KR+DLR I +IDP D+DDAL
Sbjct: 496 SKKVLECLPAEGHDWKAPTCLDDPEAVSKDPLLT KRKDLRDKLICSIDPPGCV DIDDALH 555

Query: 394 CRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSL 453
++L +G +EVGVHIADV++FV G++LD A R TSVYLV K + MLP LL +LCSL
Sbjct: 556 AKKL PNGNWEVGVHIADVTHFVKPGTALDAEGAARGTSVYLVDKRIDMLPMLLGTDLCSL 615

Query: 454 NPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXX 513
P D+ FSVIW+L I+ F +++IRS SY+ AQ I++
Sbjct: 616 KPYVDRFAFSVIWELDDSANIVNVNFMKSVIRSREAFSYEQALRIDDKTON----- 667

Query: 514 XXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIY 573
+E+ + L ++ +L+++R GAL L ++ +D ET P I +
Sbjct: 668 -----DELTMGMRALLKLSVKLKQKRLEAGALNLASPEVKVHMDSETSDPNEVEIKKL 720

Query: 574 RDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCD-QMGLPMDV 632
+N LVEEFMLLAN++VA KI+ FP+ A+LRRH P + L E + + + + +
Sbjct: 721 LATNSLVEEFMLLANISVARKIYDAFPQTAMLRRAAPPSTNFEILNEMLNTRKNMSISL 780

Query: 633 SSAGALNKSLTKTFG-DDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNV 691
S+ AL SL + +D Y ++ M +R M A YF SG FRHY L V
Sbjct: 781 ESSKALADSLDRCVDPEDPYF---NTLVRIMSTRCMMAAQYFYSGAYS-YPDFRHYGLAV 836

Query: 692 PLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD--TLQKQADHCNDRRMASKRVQE 749
+YTHFTSPIRR+ DV+ HR LA A+GY D + + N + ++
Sbjct: 837 DIYTHFTSPIRRYCDVVAHRQLAGAIGYEPLSLTHRDKNKMDMICRNINRKHNAQFAGR 896

Query: 750 LSIGLFFAVLVKESGPLESEAMVMGVNLQAQFDVLVLRFGVQ 790
SI + +++ + E+ V+ V N VLV +FGV+
Sbjct: 897 ASIEYYVGQVMRNNESTET-GYVIKVFNNGIVVLVLPKFGVE 936

>gi|21297331|gb|EAA09476.1| ebiP3704 [Anopheles gambiae str. PEST]
Length = 965

Score = 313 bits (803), Expect = 6e-84
Identities = 228/691 (32%), Positives = 352/691 (50%), Gaps = 62/691 (8%)

Query: 180 NTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPI-----PQDTRGLSEKSLQK-SAKV 233

N + VDG P+ + S V+ DE T P T + ++ ++ +AKV
 Sbjct: 280 NLNRAVDGDTVAIEMLPESSEWKAPSDVVLVDEQTDPGDMVEPDPTFSVKPQAEREPTAKV 339
 Query: 234 VYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD 293
 V I+++K R GIL + S +F P++ ++PRI + +
 Sbjct: 340 VGIKRKW-RQYCGILLPSHIQGS----TRHIFVPAERKIPRIRIETRQ----- 383
 Query: 294 FANTLFICRII----DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEV 349
 A TL RII W + G ++LG G E E E IL E+ V S FS +V
 Sbjct: 384 -AATLLSQRIIVAIQWPRHSRYPQGHFVRALGPIGSKETENEVILLEDVPHSRFSEDV 442
 Query: 350 LECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIA 409
 L CLP+ LPWTI ++ +R DLR + ++DP D+DDAL RRL +G EVGVHIA
 Sbjct: 443 LACLPE-LPWTITAADLQRRVLDLRDITVCSVDPPGCTDIDDALHARRLPNGNIEYGVHIA 501
 Query: 410 DVSFYFVEGSSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLT 469
 DV +F+ G++LD+ AA RAT+VYLV K + M+P LL LCSL ++ FS IW+L
 Sbjct: 502 DVGHFIRPGTALDREAASRATTVYLVDKRIDMVPGLLSSNLCSLRGGEERFAFSCIWELD 561
 Query: 470 PEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529
 E I + +++I+S + L+Y+ AQ +I++ +V ++
 Sbjct: 562 DEANIRNTRYHKSVIKSKSALTYEEAQIIDD-----AKQTNDVATSLRL 606
 Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
 L+ +AK L+++R GAL L ++ F +D ET P + ++N +VEEFMLLAN+
 Sbjct: 607 LNRLAKILKKRRTKEGALVLASPEIRFQVDSETHDPIDVKAKQLLETNSMVEEFMLLANV 666
 Query: 590 AVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDQGLPMDVSSAGALNKSLTKTFGDD 649
 +VA KI + FPE A+LRRHP P LV+ + G + +S L SL K D
 Sbjct: 667 SVAEKIEQEFPECAMLRRHPCPPQANYEPLVKAAEHQGFELTTSGKELATSLDKAVKPD 726
 Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIV 709
 +L + +R M A+YF SG +Q +++F HY L P+YTHFTSPIRR+AD+IV
 Sbjct: 727 NPYF--NTMLRILATRCMMQAVYFISGTQV-RDEFFHYGLAAPIYTHFTSPIRRYADIIV 783
 Query: 710 HRLLAALGYSEQPDVEPDTLQKQADH--CND---RRMASKRVQELSIGLFFAVLVKESG 764
 HRLLA +G P+ L K+ + CN+ R ++ S+ L + ++
 Sbjct: 784 HRLAACIGADS---TYPELLDKKVNNSLNNLNRYNRMAQYAGRASVALHTHLFFRKRS 840
 Query: 765 PLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824
 + +A ++ + A +LV ++G + IY R+ K G + V++ +
 Sbjct: 841 E-DEQAYILFIRKNALQILVPKYGFEGTIYVTG--RNNEEIKTGVR----FVYDEEQQT 892
 Query: 825 EEPTQQVITIFSLVDVVLQAEATALKYSAIL 855
 + Q V F V V L ++T +++ ++
 Sbjct: 893 QRCGQVVFRAFDPVIVRLSLDSTNVQHEKLV 923

Score = 53.1 bits (126), Expect = 2e-05
 Identities = 23/75 (30%), Positives = 46/75 (61%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
 +F ++++ + EG+K G L+QG + + + E ++ ++ + I G + NRA++G
 Sbjct: 228 LFPSHLTMLQIHEGIKGGKLMQGGFLASRENYLEGYVRVEGIEKAVLIQGRMNLNRAVDG 287
 Query: 109 DLVVVKLLPEDQWKA 123
 D V +++LPE +WKA
 Sbjct: 288 DTVAIEMLPESSEWKA 302

>gi|14250908|emb|CAC39259.1| Rrp44p homologue [Trypanosoma brucei]
 Length = 972

Score = 313 bits (801), Expect = 1e-83
 Identities = 187/536 (34%), Positives = 289/536 (53%), Gaps = 35/536 (6%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324
 LF P D+R+PRI + D + I DW E +F +G + LG
 Sbjct: 396 LFQPKDNRIPIRIT-----TAHLGDLKDKRLSVIIDWGEHSSFPVGHYVEVLGTI 447

Query: 325 GEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPST 384
 G+ + E + IL E + DFS V +CLP+ W + +E+G R DLR C+ ++DP
 Sbjct: 448 GDKDTEAKVILLENLIPHYDFSEAVYDCLPKG-EWNVTEELGNRLDLRLDCVVSVDPLG 506

Query: 385 ARDLDDALACRRLTDGTFEYGVHIAVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPR 444
 RD+DDAL CRR+ EVGVHIAV++F+ EG+++D+ AA+R+TSVYLV + + MLP+
 Sbjct: 507 CRDIDDALHCRVNGNHLEVGVIADVTHFLKEGTAMDEEAAKRSTSVYLVDRRINMLPQ 566

Query: 445 LLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXX 504
 LL E LCS+ D+ FS++W+ ++ E+FG+T+IRS L Y AQ MI++
 Sbjct: 567 LLTENLCSIVADEDRYAFSIMWEFDENYSVVREFFGKTVIRSRAALYYGDAQRMIDDPED 626

Query: 505 XXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGL 564
 E ++ L +++ R++R DGAL L + F +D++
 Sbjct: 627 E-----SEAAVSLRYLMQLSRHFRKRREKDGALFLCSQEFKFKVDNDHVN 671

Query: 565 PQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFC- 623
 P Y+ DSN ++EE+ML AN A A +++ +FP LLRRH P L E
 Sbjct: 672 PTDMQAYQTFDSNSMIEEWMLFANAAAARRVYASFPRWTLRRHQAPAENAFDTLNEAIR 731

Query: 624 DQMGLPMDVSSAGALNKSILTFTGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQ 683
 ++G+ +D +++ ALN+SL K R ++ + +R ++ A YF S + +++
 Sbjct: 732 RKIGVKLDDTTSLALNESLEKCVDPSPDYFNR--LIRTLVTRCLRQAQYFSSSEVS-KDE 788

Query: 684 FRHYALNVPLYTHFTSPIRRFADVIVHRLAALGYSEQPDVEPDTLQKQ--ADHCNDRR 741
 F H+ L +P+YTHFTSPIRR+ADVIVHR LAAALG + + +++ + A + N R
 Sbjct: 789 FHHFGLAMPIYTHFTSPIRRYADVIVHRQLAALGIMDVSEAHMVSVKMEALASNLNYRH 848

Query: 742 MASKRV---QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRI 793
 ++R Q L G + + P E +V F VLV ++G + +I
 Sbjct: 849 EQAQRAGRDSQNLFTGFYLRNFANQEIPSEDGYVVKLSETHVF-VLVPKYGQEGKI 903

Score = 40.0 bits (92), Expect = 0.17

Identities = 26/115 (22%), Positives = 52/115 (45%), Gaps = 9/115 (7%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGD-----RDIFIDGVVAR 102
 +F +++++ + G++ GT ++G LR++ F G + + G
 Sbjct: 235 LFSPHLAESALDLGVQNGTYLRGKL RVSETN---CFFGEIRGQWKGNFERNVLLPGRTNL 291

Query: 103 NRALNGDLVVVKLLPEDQWKAVKPESNDKEIATYEADIPEEGCGHHPLQQSRKG 157
 NRA++GD+V V+LLP W+ ++ +E+ T E G + + +G
 Sbjct: 292 NRAIHGDIIVTELLPVASWRPLRGAKPTEEMNDTGAGGDDHENSREGIGEESEG 346

>gi|19113445|ref|NP_596653.1| mitotic control protein dis3
 [Schizosaccharomyces pombe]
 gi|585053|sp|P37202|DIS3_SCHPO Mitotic control protein dis3
 gi|283075|pir||A41944 mitotic control protein dis3+ - fission yeast
 (Schizosaccharomyces
 pombe)
 gi|173381|gb|AAA35302.1| mitotic control protein
 gi|3650393|emb|CAA21102.1| mitotic control protein dis3
 [Schizosaccharomyces pombe]
 Length = 970

Score = 301 bits (770), Expect = 4e-80

Identities = 202/594 (34%), Positives = 301/594 (50%), Gaps = 43/594 (7%)

Query: 218 DTRGLSEKSLQKSAKVYVILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIY 277
 D +++++ +AKVV IL++ + ++ ++ L +P D RVP+I
 Sbjct: 348 DLELITKRNAHPTAKVVIGILKRNWRPYVGHVDNATIAQSKGGSQQTVLLTPMDRRVVKIR 407

Query: 278 VPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337
+ P+ R + I W + G + LG+ E ETE +L E
Sbjct: 408 FRTRQAPRLVGRR-----IVVAIDLWDASSRYPEGHFVRDLGEMETKEAETEALLLE 459

Query: 338 YGVDFSDFSSEVLECLPQS-LPWTIPPDEV----GKRRDLRKDCIFTIDPSTARDLDDAL 392
Y V F VL+CLP+ W +P D+ R+D R I +IDP +D+DDAL
Sbjct: 460 YDVQHRPFPKAVLDCLPEEGHNWKVPADKTHPLWKNRKDFRDKLICSIDPPGCQDIDDAL 519

Query: 393 ACRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLICEELCS 452
L +G +EVGVHIADV++FV +S+D AA R T+VYLV K + MLP LL +LCS
Sbjct: 520 HACVLPNGNYEVGVHIADVTHFVKPNTSMDSEAASRGTTVYLVDKRIDMLPMLLGTDLCS 579

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXXX 512
L P ++ FS IW++ I++ F +++I S SY AQ+ I++
Sbjct: 580 LRPYVERFAFSCIWEMDENANI IKVHFTKSVIASKEAFSYADAQARIDDQKMQ----- 632

Query: 513 XXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYE 572
+ + Q + L ++K L+++R +GAL L ++ D+ET P I +
Sbjct: 633 -----DPLTQGMRVLLKLSKILKQKRMDEGALNLASPEVRIQTDNETSDPMDVEIKQ 684

Query: 573 YRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH-PPPQTKM--LSDLVEFCDQMGLP 629
++N LVEEFMLLAN++VA KI+ FP+ A+LRRH PP T L D++ C M L
Sbjct: 685 LLETNSLVEEFMLLANISVAQKIYDAFPQTAVLRRHAAPPLTNFDSLQDILRVCKGMHLK 744

Query: 630 MDVSSAGALNKSLTKTFGD--DKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY 687
D S KSL K+ + D +L + +R M A YFCSG + FRHY
Sbjct: 745 CDTS-----KSLAKSLDECVPKEPYFNTLLRILTTTRCMLSAEYFCSGTFAPPD-FRHY 797

Query: 688 ALNVPLYTHFTSPIRRFADVIVHRLLAALGYSE-QPDV-EPDTLQKQADHCNDRRMASK 745
L P+YTHFTSPIRR+ADV+ HR LAAA+ Y P + + L + + N R ++
Sbjct: 798 GLASPIYTHFTSPIRRYADVLAAHRLAAIDYETINPSLSDKSRLEICNGINRHRMAQ 857

Query: 746 RVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAQFDVLVLRFGVQKRIYCNALA 799
SI + +K G E +A V+ V F V + RFG++ +Y +L+
Sbjct: 858 MAGRASIEYYVGQALK-GGVAEEDAYVIKVFKNQGVVFIARFGLEGIVYTKSLS 910

Score = 49.7 bits (117), Expect = 2e-04
Identities = 23/84 (27%), Positives = 46/84 (54%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
++E + S + +K G + +G++ I+ + E + P ++ + + G NRA+ G
Sbjct: 247 VYELHWSMSRLLACIKNGEVHKGLINISTYNYLEGSSVVVPGYNKPVLVSGRENLRNAVQG 306

Query: 109 DLVVVKLLPEDQWKAVKPESNDKE 132
D+V +++LP+DQWK E D +
Sbjct: 307 DIVCIQILPQDQWKTEAEIADDD 330

>gi|15021874|dbj|BAB62212.1| hypothetical protein [Macaca fascicularis]
Length = 249

Score = 291 bits (745), Expect = 3e-77
Identities = 156/247 (63%), Positives = 171/247 (69%), Gaps = 2/247 (0%)

Query: 1 MNHPDYKLNLRXXXIFETYMSKEDVS 60
M+HPDY++NLR D IFETYM KEDVS
Sbjct: 1 MSHPDYRMNLRPLGTGPRGVSTVAGPHGIGASPGDKKSKNKSTRGKKKSIFETYMFKEDVS 60

Query: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPE+Q
Sbjct: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEEQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS-GPDVIEAQFDDSDSEDRHG 179
WK VKPE+NDKE EA YE+DIPEE CG H QQS K ++ PDVIEAQFD SDSED HG

Sbjct: 121 WKVVKPENNDKETEAAYESDIPEELCGRHLPQQSLKSYNDSPDVIIIEAQFDGSDSEDGHG 180
Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILE 238
T LVD VKKLS+ ++G+E PV KDE T I QDTR L EKSLQ+SAKV+
Sbjct: 181 ITQNVLVDDVKKLSVCVSEKGREHGDAPVTKDETTTCISQDTRALPEKSLQSAKVIAYRF 240
Query: 239 KKHSRAA 245
H + A
Sbjct: 241 SSHVQMA 247

>gi|19115966|ref|NP_588616.1| hypothetical protein MGC4562 [Homo sapiens]
gi|18314381|gb|AAH22089.1|AAH22089 Similar to mitotic control protein dis3
homolog [Homo sapiens]
Length = 971

Score = 284 bits (727), Expect = 4e-75
Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + QDF + RI W+ + G + LG
Sbjct: 283 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 332
Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F
Sbjct: 333 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEQKRKDLRKSHLVF 392
Query: 379 TIDPSTARDLDDALACRRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 393 SIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 452
Query: 439 VPMLPRLLCHEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 453 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEEAAQE 512
Query: 498 MIENXXXXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++
Sbjct: 513 LLDGNLSVVDDIPEFKDLDEKSRQAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 572
Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H
Sbjct: 573 VCVQLDDKKNIHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 626
Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQ 668
PPP + S+L E G +D S L SL +D + +L +M ++ M
Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDN--ANDPHDPIVNRLLRSMATQAMS 684
Query: 669 MALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD 728
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLLAALGYSEQPDVEPD
Sbjct: 685 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSDIVVHRLLMALSKDKKMEIKGN 743
Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLE-----SEAMVMGVLNQ 778
L++ H N+R A++ Q+ S LF + K+ P S+ ++ +
Sbjct: 744 LFSNKDLEELCRHINNRRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIIYSIRTN 803
Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824
+ + RFG++ Y L++ + P+ W+P L+
Sbjct: 804 GVLLFIPRFGIKGAAY-----LKNKDGLVISCGPDSCSEWKPGSLQ 844

Score = 59.3 bits (142), Expect = 3e-07
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101
+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A
Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKSDLVSDILIHGMKA 201

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
RNR+++GD+VVV+LLP+++WK
Sbjct: 202 RNRSIHGDVVVVVELLPKNEWKG 223

>gi|18916779|dbj|BAB85541.1| KIAA1955 protein [Homo sapiens]
Length = 947

Score = 284 bits (726), Expect = 5e-75
Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + QDF + RI W+ + G + LG
Sbjct: 259 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 308

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F
Sbjct: 309 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEEQKRKDLRKSHLVF 368

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVIADVSFYFPEGSSLDKVAAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 369 SIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 428

Query: 439 VPMLPRLLCCELCSLNPMTDKLTFSVIWKLTPGEG-KILEEWFGRRTIIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 429 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEEAAQE 488

Query: 498 MIENXXXXXXXXXXXXXXXXXHS---VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++
Sbjct: 489 LLDGNLSVVDDIPEFKDLDEKSRQAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 548

Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H
Sbjct: 549 VCVQLDDKKNIHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 602

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQ 668
PPP + S+L E G +D S L SL +D + +L +M ++ M
Sbjct: 603 PPPHQEFFSELRECAKAKGFFIDTRS NKT LADSLDN--ANDPHDPIVNRLLRSMATQAMS 660

Query: 669 MALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL LAAALGYSEQPDVEPD 728
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRL L AA+ ++ +++ +
Sbjct: 661 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYS DIVVHRL LMAAISKDKKMEIKGN 719

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLE-----SEAMVMGVLNQ 778
L++ H N+R A++ Q+ S LF + K+ P S+ ++ +
Sbjct: 720 LFSNKDLEELCRHINN RNQAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIYSIRTN 779

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824
+ + RFG++ Y L++ + P+ W+P L+
Sbjct: 780 GVLLFIPRFGIKGAAY-----LKNKDGLVISCGPDSCSEWKPGSLQ 820

Score = 59.3 bits (142), Expect = 3e-07
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101
+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A
Sbjct: 118 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKDSDLVSDILIHGMKA 177

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
RNR+++GD+VVV+LLP+++WK
Sbjct: 178 RNRSIHGDVVVVVELLPKNEWKG 199

>gi|27369724|ref|NP_766107.1| hypothetical protein 4932411M14 [Mus musculus]

gi|26325912|dbj|BAC26710.1| unnamed protein product [Mus musculus]
Length = 970

Score = 283 bits (724), Expect = 9e-75
Identities = 194/595 (32%), Positives = 300/595 (50%), Gaps = 50/595 (8%)

Query: 265 LFSPSDHRVPRIYVPLK--DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + + QDF + RI W+ + G + LG
Sbjct: 283 LVTPWDYRIPKIRISTQQAEALQDFRV-----VVRIDSWEATSVYPNGHFVRVLG 332

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRDK-CIF 378
+ G++E E IL E + FS + +P + PW + P E +R+DLR +F
Sbjct: 333 RIGDLEGEIATILVENSISVVPFSEAQMCEMPVNTPENPWKVPKKEEQERKDLRTTHLVF 392

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 393 SIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDVEARTRATTYYLADDR 452

Query: 439 VPMLPRLLCHEELCSLNPMTDKLTFSVIWKLTPG-KILEEWFGRITIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ SV+W+L +I + W+GRITIRS KL Y+ AQ
Sbjct: 453 YDMLPSILSADLCSLLGGVDRYAVSVMWELDKTSYEIKKVWYGRITIRSAYKLFYEAQAE 512

Query: 498 MIENXXXXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++
Sbjct: 513 LLDGNFSIVDDIPELKALDKQSQAQKLEELVWAIGKLTDIARHIRAKRDRCGALELEGVE 572

Query: 554 LAFTLDHETGL-----PQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
+ LD + + Q ++E V E M+LAN VA KI+ +FP QALLR+H
Sbjct: 573 VRVQLDDKKNIRDLPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 626

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQ 668
PPP + S+L E G +D S L SL D K L K +L +M ++ M
Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNTLADSLDSA-NDPKDPLVNK-LLRSMATQAMS 684

Query: 669 MALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD 728
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLLA A+ ++ +++ +
Sbjct: 685 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSDIVHRLLMAAISKDKKMEIKEN 743

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE-----AMVMGVLNQ 778
L++ H N+R A++R Q+ S LF + K+ E ++ +
Sbjct: 744 LFSNKNLEELCRHINNRRNAAQRSQKQSTELFQCMYFKDRDAETEERCIADGVIYSIRTN 803

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWEPDDLEEEPTQQVIT 833
V + RFG++ Y L++ + PE + W+P L+ + + T
Sbjct: 804 GVLVFIPRFGIKGAAY-----LKNKDSLVISCGPEGSSSEWKPGSLQRSQNKIIST 853

Score = 54.7 bits (130), Expect = 7e-06
Identities = 33/103 (32%), Positives = 54/103 (52%), Gaps = 8/103 (7%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101
+ ++ E + G+K G IQG+L +N + EAF+ S D DI I G A
Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLHGASSKDSGLVSDILIHGSKA 201

Query: 102 RNRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144
RNR+++GD+VVV++LP+ +WK + + + + P E
Sbjct: 202 RNRSIHGDVVVVEMLPKSEWKGRTAALGENSDDKASGESPE 244

>gi|14250916|emb|CAC39263.1| putative ribonuclease II-like protein
[Trypanosoma brucei]
Length = 895

Score = 278 bits (710), Expect = 4e-73
Identities = 236/763 (30%), Positives = 352/763 (46%), Gaps = 109/763 (14%)

Query: 52 TYMSKEDVSEGLKRGTLIQGLRI-NPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDL 110
T S ++ + +K G ++ G LR+ + AF+ S D+ + G + NR L+ D+
Sbjct: 18 TIGSNPEMEKQVKHGCVVIGRLRVYSSYNSGLAFVRS GAFFPADVVVKGYGSINRFLHNDV 77

Query: 111 VVVKLLPEDQWKAV-----KPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVII 165
V V+LLP +QW+ V +P+ +DK+ T D L R+ I
Sbjct: 78 VAVQLLPMEQWEDVVS GELEPDGDDKDEFRTMRPD-----SERLPDGRR-----I 122

Query: 166 EAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEK 225
D+ +R L + +S P P
Sbjct: 123 TRWIRDTTMNNRKNREMWLAE-----MMSAPTEHNWHGKKP----- 158

Query: 226 SLQKSAKVVIILEKKHSRAATGILKLLADKNSDLF--KKYALFSPSDHRVPRIYVPLKDC 283
S V+ +LE+KH L A + ++ +++ F D +P I V +D
Sbjct: 159 ----SGSVIAVLERKHPLLFVARLADDALSSQEVIQDRRFYRFKVFQDLLPHIAVFGRDI 214

Query: 284 PQDFMTRPKDFANTLFICRI-----IDWKEDCNFALGQLAKSLGQAGEIEPETEGILT 336
P F R + ++ R+ I W E F ++ + G + T I +
Sbjct: 215 P--FSLR-ESIRERFYLLRLETTTGGDIVWAES-RFPTARIISTFGSVHSLRANTFAICS 270

Query: 337 EYGVDFSDFSSEVLECLPQSLPWTIPPDEVGK--RRDLRK-DCIFTIDPSTARDLDDAL 392
+ + DFS E C+P L IP E K RDLR+ + + +IDP+TARDLDDAL
Sbjct: 271 AHHIVTDDFSEEACNCIPDRL--IIPNSEEMKRTGRDLRREEFVCSIDPATARDLDDAL 328

Query: 393 ACRRITDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCS 452
+ L G + VGVHIADVS+V GS+LD+ RATSIVLV +V MLPR L EE CS
Sbjct: 329 SI-TLLPGGYRVGVHIADVSHFVSPGSALDEEGRARATSVYLVDRVYHMLPRKLSEELYCS 387

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXX 512
L+P +DKL FS I++L GK+ EWFG+++IR+ +LSYD AQ +I+
Sbjct: 388 LHPGSDKLAFSAIFQLDLNGKLGKGEWFGKSVIRNRCRLSYDDAQRIIDGNLTTLDALDYG 447

Query: 513 XXXXXHSVEE---VHQAVNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETG--LPQ 566
+ + V +V +L +A +LR F G L ++ F + + P
Sbjct: 448 GVTDRRELSQLKARVATSVKHLFDLASKLRAASFERRGLAFSTPEIGFHFEDISNPTHPI 507

Query: 567 GCHIYEYRDSNKLVEEFMMLLANMAVAHKIFRTFPEQALLRRHPPPPQTKMLSDLVEFCDQM 626
G +++ ++N LVEEFMMLAN+ VA KI + P+QA+LR HPPP+ L ++
Sbjct: 508 GFNVHRQIEANWLVEEFMMLANLRVAQKIVQYLPDQAILRVHPPPKRVPFEQL-----KV 562

Query: 627 GLP-MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGM-LQDQEQF 684
L +++ G NKSL + + R E+ + M + +A Y +G ++
Sbjct: 563 SLARVNIELKGRSNKSLEQLLNSVRDHPLRDEI-SIMVKNTLSLAKYCTNGENFTNKVPL 621

Query: 685 RHYALNVPLYTHFTSPIRRFADVIVHRLAALGYSE-----QPDVEPDTL 730
HYAL + YTHFTSPIRR+AD+IVHR L AL +E + L
Sbjct: 622 GHYALGLEWYTHFTSPIRRYADIIVHRQLLCALEIESIVKKGKRTGKTCAGAVGMEVECL 681

Query: 731 QKQ-----ADHCNDRMASKRVQELSIGLFFAVLVK 761
AD CN+ + A+ V E S+ LFF +K
Sbjct: 682 DSAEFTSTYEVMNIADECNENKRAADSVSEASLKLFFCHYLK 724

>gi|15559519|gb|AAH14124.1|AAH14124 Unknown (protein for IMAGE:4561365)
[Homo sapiens]
Length = 647

Score = 270 bits (689), Expect = 1e-70
Identities = 178/534 (33%), Positives = 276/534 (51%), Gaps = 38/534 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRD 371
G + LG+ G++E E IL E + FS + +P + PW + P+E KR+D
Sbjct: 1 GTRVRVLGRIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPEPWKVSPEEEQKRKD 60

Query: 372 LRKD-CIFTIDPSTARDLDDALACRRITDGTFEVGVHIADVSYFVPEGSSLDKVAAERAT 430
LRK +F+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT

Sbjct: 61 LRKSHLVFSIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRAT 120

Query: 431 SVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGEG-KILEEWFGRTIIRSCTK 489
+ YL + MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS K

Sbjct: 121 TYYLADRRYDMLPSVLSADLCSLLGGVDYAVSIMWELDKASYEIKKVWYGRTIIRSAYK 180

Query: 490 LSYDHAQSMIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHSLIAKQLRRQRFVDG 545
L Y+ AQ +++ S +EE+ A+ L IA+ +R +R G

Sbjct: 181 LFYEAAQELLDGNLSVVDIPEFKDLGEKSRQAKLEELVWAIGKLTDIARHVRKRDGCG 240

Query: 546 ALRLDQLKLAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMMLLANMAVAHKIFRTFP 600
AL L+ +++ LD H+ Q ++E V E M+LAN VA KI+ +FP

Sbjct: 241 ALELEGVEVCVQLDDKKNHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFP 294

Query: 601 EQALLRRHPPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLT 660
QALLR+HPPP + S+L E G +D S L SL +D + +L

Sbjct: 295 HQALLRQHPPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDN--ANDPHDPIVNRLLR 352

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720
+M ++ M ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLLAALGYS

Sbjct: 353 SMATQAMSNALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSDIVVHRLLMALISKD 411

Query: 721 EQPDVEPD-----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLE-----SEA 770
++ +++ + L++ H N+R A++ Q+ S LF + K+ P S+

Sbjct: 412 KKMEIKGNLFSNKDLEELCRHINNRRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDG 471

Query: 771 MVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824
++ + + + RFG++ Y L++ + P+ W+P L+

Sbjct: 472 VIYSIRTNGVLLFIPRFGIKGAAY-----LKNKDGLVISCGPDSCSEWKPGSLQ 520

>gi|23136616|gb|ZP_00118334.1| hypothetical protein [Cytophaga hutchinsonii]
Length = 750

Score = 265 bits (676), Expect = 3e-69
Identities = 168/466 (36%), Positives = 252/466 (54%), Gaps = 35/466 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374
G++ + LG AGE E E IL E+G+ + +F ++V++ Q + E+ KRRD+R

Sbjct: 219 GKVTEVLGMAGENETEMHAILAEFGLPY-EFPNQVIKA-AQDITAETSEAEIKKRRDMRG 276

Query: 375 DCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYL 434
FTIDP A+D DDA++ + L +G +E+GVHIADV++V G +LDK A RATSVYL

Sbjct: 277 TTTFTIDPEDAKDFDDAISFKYLDNGNWEIGVHIADVSHYVQPGDTLDKEAYRRATSVYL 336

Query: 435 VQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGEGKILEEWFGRTIIRSCTKLSYDH 494
V + VPMLP L ELCSL P DKLTFS I+++ + K+L+EWFGRTII S + SY+

Sbjct: 337 VDRCVPMLPERLSNELCSLRPNEDKLTFSAIFEIDADAKVLDEWFGRTIIHSTRRFSYEQ 396

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLIAKQLRRQRFVDGALRLDQLKL 554
AQ +IE ++ + + L+++AK++R QRF +GA+ + +++

Sbjct: 397 AQEVIETQQG-----DLVKELTILNTLAKKMRAQRFKEGAISFETVEV 439

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMMLLANMAVAHKIF-----RTFPEQALLRRHP 609
F LD + G P +D++KL+EEFMMLLAN VA +F + + R H

Sbjct: 440 KFQLDAK-GKPLAVVPKVRKDAHKLIEEFMMLLANKRVAEFVFNLRKGKGTSTNTMVYRTHD 498

Query: 610 PPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQM 669
P + L+ L F + G +++ A+ K+L K D+ + VL ++ R M

Sbjct: 499 APNPEKLASLATFAKRFHGKVELDDENAIKLNK-LSDEVEGKPEQNVLQSLAIRTMSK 557

Query: 670 ALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDT 729
A+Y E H+ L Y+HFTSPIRR+ DV+ HRL L + D E

Sbjct: 558 AIY-----SIEPDMHFGLAFKHYSHTSPIRRYPDVMARLLQHYLDGGKSADKE--Y 608

Query: 730 LQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775
+ +H + + + + SI ++ S E E +V GV
Sbjct: 609 YIEACEHSSAQEKLAEEAERSSIKFKQVEFMQSSIGKEFEGIVSGV 654

>gi|19173030|ref|NP_597581.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)
[Encephalitozoon
cuniculi]
gi|19168697|emb|CAD26216.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)
[Encephalitozoon
cuniculi]
Length = 835

Score = 260 bits (665), Expect = 6e-68
Identities = 161/460 (35%), Positives = 240/460 (52%), Gaps = 64/460 (13%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324
L P D R+P I + ++ ++ N I W+ N+ G + LG
Sbjct: 288 LVIPIDRRIPAIRIR-----TSQAEELMNKRLCVEIDGWERTSNYPSPGHYYRRLGTL 339

Query: 325 GEIEPETEGILTEYGVDFSDFS-SEVLECLPQSLPWTIPP-----DEV--GKRRDLR 373
G+ E E +L G+ + + + +E+L +PW +EV G R D R
Sbjct: 340 GDRNAEMEAVLVANGITYYNKNWAEILR-----VPWMNEDIFGMEKAYNEVREGTREDFR 394

Query: 374 KDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVY 433
+ I +IDP D+DDAL CR L +G +EVGVHIADV+Y+V +GS +DK+AA+R T++Y
Sbjct: 395 ELSIVSIDPPDCEDIDDALHCRLLPNGNWEVGVHIADVITYYVTKGSEIDKIAADRGTITIY 454

Query: 434 LVQKVVPMLPRLLCSEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYD 493
L + + MLP L +LCSL D+ FSV+W+++ + +++ F R++IRS SY+
Sbjct: 455 LPEWRIDMLPPLSTDLC SLVAGKDRAAFSVVWEMSSDVRVVRTHFCRSLIRSKRSFSYN 514

Query: 494 HAQSMIENXXXXXXXXXXXXXXXXXXXXHSEVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
A ++ +EV +++ L I++ LR +RF G+L L +
Sbjct: 515 EAYDAVQGLVDAG-----DEVSRSLRMLLEISRVLSRRFAKGS LLDLSTRQ 560

Query: 554 LAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQT 613
L F G + EY +N LVEEFM+LAN++VA I+ P+ +LLR+HPPP
Sbjct: 561 LVFR-----EGGFEMKEYFPTNFLVEEFMVLANISVASFIYHHHPDSSLLRKHPPPSV 613

Query: 614 KMLSDLVEFCQDQMG LPM DVSSAGALNKSLTKTFGDDKYSLARKEVL TNMYSRPMQMALYF 673
+GL +D SS AL++SL K G RK++ M R M A+Y
Sbjct: 614 L-----DIGLDIDTSSPRALSESLEKMEG-----VRKDLAKRMLIRSMNQAVYV 657

Query: 674 CSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713
SG + HY L P+YTHFTSPIRR+AD+IVHR+L
Sbjct: 658 VSG---ETPSLHHYGLATPIYTHFTSPIRRYADIIVHRIL 694

>gi|7493807|pir||T30524 protein phosphatase Ssd1 homolog - yeast (Candida albicans)
gi|2459997|gb|AAC83386.1| protein phosphatase Ssd1 homolog [Candida albicans]
Length = 1262

Score = 246 bits (628), Expect = 1e-63
Identities = 230/859 (26%), Positives = 391/859 (45%), Gaps = 86/859 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQVLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106
+F Y+ + + E + G L+ G LR+N K +A++ S DG D DIFI G RNRAL
Sbjct: 336 LFAPYLPQSSLP ELINEGRLVTGTLRVNKKNRSDAYV-STDGLLDADIFICGSKDRNRAL 394

Query: 107 NGDLVVVKLLPEDQ-WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVII 165
GDLV V+LL D+ W++ K + K + P H+ S P+
Sbjct: 395 EGD LVAVELLIVDEVWESKKEKEEKKRRKDNTLHSRPLTDDIHN-----DATSAPNT-A 447

Query: 166 EAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIP-QDTRGLSE 224

E + ED G+ G+ + RG + K+++ + Q + E
 Sbjct: 448 EGSVTGTSKEDGAGSNEEETGGLAR-----RGS LKQRPTMKKNDDVEVEGQSLLLLVEE 500
 Query: 225 KSLQKSAK-----VVYILEKKHSRAATGILKLL-----ADK-----NSDLFK 261
 + + K VV +++++ + G L LL DK +
 Sbjct: 501 EEINDEIKPLYAGHVAVVDRI PGQLFAGTLGLLRPAQAAQAARDKKNGKESTVQNPKAP 560
 Query: 262 KYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSL 321
 K F P+D +VP I +P + P+DF+ + +A+ LF+ I W G L +L
 Sbjct: 561 KIVWFKPTDKKVPLIAIPTEQAPKDFVENHEKYADRLFVASIKRWPITSLHPFGTLVSNL 620
 Query: 322 GQAGEIEPETEGILTEYGVDFSDFS----SEVLECLPQSLPWTIPPDEVGKRRDLRKDCI 377
 G E E + IL + ++ +++ LP P E +R + D I
 Sbjct: 621 GPIDSPETEIDSILRDNNFLCDEYPDDDNDNDIVSVNAYDLPSIEPEFENTQREEYLNDYI 680
 Query: 378 FTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQK 437
 +D AL +R+++ E+G H+AD++YF+ GSSLD+ + +R++SV+L QK
 Sbjct: 681 IAFT-QNGEFVDHALHVKRISNTKIELGFHVADIAYFIKPGSSLDKSKKRSSSVFLPQK 739
 Query: 438 VVPMPLPRLLCEELCSLNPMTDKLTFSVIWKL-TPEGKILEEWFGRTIIRSC TKLSYDHAQ 496
 V + P+ + ++ S L SV++++ T ++ + + ++I ++YD
 Sbjct: 740 TVNLFPKQV-NKIVSFKENEKNLAVSVVFEIDTSNFEVEDLYIHESVIIPKQLV TYDAFD 798
 Query: 497 SMIENXXXXXXXXXXXXXXXXXHSVEEVHQA----VLNLHSIAKQLRRQRFVDGALRLD-Q 551
 +++ SV+ + A V IAK+ RR R + +L +
 Sbjct: 799 TILSG-----QSVDSISSATSDYVKTFSLIAKEFRRHRLSNRSLGITPN 842
 Query: 552 LKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611
 L L LD E + +I++ + ++ E N A+A K+ +QA+LRRHP P
 Sbjct: 843 LTLLDQLDDEK-VRLDLNIFKDSLAFD VISEISHKVNSAIAAKVHAGLGDQAILRRHPLP 901
 Query: 612 QTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVL TNMYSRPMQMAL 671
 + + V +G +D +++ L S+ K DD + RK V T +Y + M
 Sbjct: 902 TLQKMETFVRKATSLGFKIDTTTSSTLQNSILKI--DD--PVKRKCVETLLY-KCMSRGR 956
 Query: 672 YFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL LAAALGYSEQPDVEPDTLQ 731
 Y+ +G QD + + HY N+PLYTHFT+P+RR+AD+IVHR L A L + D + D+L+
 Sbjct: 957 YYVAGK-QDTSYAHYYFNLPLYTHFTAPLRRYADLIVHRQLKAVLN-KQVEDKDLD SLK 1014
 Query: 732 KQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV LNQ----AFDVLVLR 787
 D+CN ++ + QE +I L + + E + + MG + Q +FDV + F
 Sbjct: 1015 AITDYCNFKKDCAANAQEQA IHL LLSQTINEMSETAGQLLCMGT VVQVYESSFDVFIPEF 1074
 Query: 788 GVQKRIYCNALALRSYSFQKVGKKPELTLVWEP--DDLEEEPTQQVITIFSLVDVVLQAE 845
 GV+KR++ + L L F K + L L WE D P + ++ + +
 Sbjct: 1075 GVEKRVHGDQLPLVKA EFDK--NERILELWWEKGVDSATYIPPDEKSSLSYRNSIKNKYR 1132
 Query: 846 ATALKYSAILKRPGLEKAS 864
 +AL+ + I + LEK++
 Sbjct: 1133 TSALQAAKIQSKTALEKST 1151

>gi|22748821|ref|NP_689596.1| hypothetical protein MGC42174 [Homo sapiens]
 gi|20988352|gb|AAH30113.1| similar to Hypothetical 93.7 kDa protein
 F48E8.6 in chromosome III
 [Homo sapiens]
 Length = 159

Score = 242 bits (617), Expect = 2e-62
 Identities = 119/135 (88%), Positives = 127/135 (94%)

Query: 727 PDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV LNQAFDVLVLR 786
 PDTLQKQADHCND RMASKRVQELS LFFAVLVKESGPLESEAMVMG+L QAFDVLVLR
 Sbjct: 3 PDTLQKQADHCNDSRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQAFDVLVLR 62
 Query: 787 FGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEA 846

+GVQKRIYCNALALRS+ FQKVGKKPELTLVWEP+D+E+EP QQVITIFSLV+VVLQAE
Sbjct: 63 YGVQKRIYCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPAQQVITIFSLVEVVLQAEY 122

Query: 847 TALKYSAILKRPGLE 861
TALKYSAILKRPG +
Sbjct: 123 TALKYSAILKRPGTQ 137

>gi|27685983|ref|XP_237349.1| similar to hypothetical protein MGC37640 [Mus
musculus] [Rattus
norvegicus]
Length = 1034

Score = 241 bits (614), Expect = 5e-62
Identities = 117/128 (91%), Positives = 121/128 (94%), Gaps = 2/128 (1%)

Query: 188 VKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIILEKKHSRAATG 247
+KK+S S+ DR KEDSS PVMKDENTP QDTR LSEKSLQKSAKVVIILEKKHSRAATG
Sbjct: 509 LKKIS-SSNDR-KEDSSAPVMKDENTPKSQDTRALSEKSLQKSAKVVIILEKKHSRAATG 566

Query: 248 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWK 307
ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD+ANTLFICRIIDWK
Sbjct: 567 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDYANTLFICRIIDWK 626

Query: 308 EDCNFALG 315
EDCNFALG
Sbjct: 627 EDCNFALG 634

Score = 142 bits (357), Expect = 3e-32
Identities = 64/80 (80%), Positives = 70/80 (87%)

Query: 122 KAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQFDDSDSEDRHGNT 181
+ VKPESNDKE EAT E DI EE CGHH LQ+S KGW+GPDVIEAQFDDSDSEDRHGNT
Sbjct: 328 RGVKPESNDKETETATNETDISEESCGHHLLQKSPKGWNGPDVIEAQFDDSDSEDRHGNT 387

Query: 182 SGLVDGVKKLSISTPDRGKE 201
SGLVDG+KKLS+ TPD+G E
Sbjct: 388 SGLVDGMKKLSVCTPDKGSE 407

Score = 127 bits (320), Expect = 6e-28
Identities = 58/62 (93%), Positives = 60/62 (96%)

Query: 316 QLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRDK 375
QLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPP+EVGKRRDLR
Sbjct: 724 QLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPEEVGKRRDLRSL 783

Query: 376 CI 377
C+
Sbjct: 784 CL 785

Score = 117 bits (292), Expect = 9e-25
Identities = 52/57 (91%), Positives = 57/57 (100%)

Query: 68 LIQGVLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGDLVVVKLLPEDQWKAV 124
+++GVLRLINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGDLVVVKLLPEDQWK++
Sbjct: 205 VLKGVLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGDLVVVKLLPEDQWKSL 261

Score = 60.1 bits (144), Expect = 2e-07
Identities = 25/28 (89%), Positives = 28/28 (100%)

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDG 400
+KDCIFTIDPSTARDLDDAL+CR+LTDG

Sbjct: 867 QKDCIFTIDPSTARDLDDALSCRQLTDG 894

>gi|6320499|ref|NP_010579.1| Product of gene unknown; Ssd1p [Saccharomyces cerevisiae]

gi|134917|sp|P24276|SSD1_YEAST SSD1 PROTEIN (SRK1 PROTEIN)

gi|101639|pir||A39578 SSD1 protein - yeast (Saccharomyces cerevisiae)

gi|172612|gb|AAA35047.1| SSD1 protein

gi|172697|gb|AAA35089.1| SRK1

gi|1230657|gb|AAB64469.1| Ssd1p [Saccharomyces cerevisiae]

Length = 1250

Score = 221 bits (564), Expect = 3e-56

Identities = 227/823 (27%), Positives = 369/823 (44%), Gaps = 95/823 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106
+F Y+ + ++ E ++ G L+ G+LR+N K +A++ S DG D DI+I G RNRAL
Sbjct: 340 LFAPYLPQANIPELIQEGR LVAGILRVNKKNRSDAWV-STDGALDADIYICGSKDRNRAL 398

Query: 107 NGDLVVVKLL-PEDQWKA-VKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVI 164
GDLV V+LL +D W++ + E + +A+ + D+ PL S + V
Sbjct: 399 EGD LVAVELLVDDVWESKKEKEEKRRKDASMQHDLI-----PLNSSDDYHNDASVT 451

Query: 165 IEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPV-----MKDENTPI 215
+ S + S V++ ST + + S+P +K T
Sbjct: 452 AATSNNFLSSPSSSDSLSKDDL SVRRKRSSTINNDSDSLSSPTKSGVRRRSSLKQRPTQK 511

Query: 216 PQDTRGLSEKSL-----QKSAKVYILEKKHSRAATGILKLL--ADKNSD 258
D + +SL + VV +L++ + +G L LL NSD
Sbjct: 512 KNDDVEVEGQSLLLVEEEEINDKYKPLYAGHVAVLDRI PGQLFSGTLGLLRPSQQANS 571

Query: 259 LFK-----KYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFA 313
K K A F P+D +VP I +P + P+DF+ ++ LF+ I W
Sbjct: 572 NNKPPQSPKIAWFKPTDKKVPLIAIPTELAPKDFVENADKYSEKLFVASIKRWPITSLHP 631

Query: 314 LGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLEC-----LPQSLPWTIPPDEVG 367
G L LG + + E + IL D + S+E L+ P P + + +
Sbjct: 632 FGILVSELGDIHDPDTEIDSILR---DNNFLSNEYLDQKNPQKEKPSFQPLPLTAESLE 687

Query: 368 KRR---DLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKV 424
RR D + IF I + AL R +GT E+G H+ DV+ + EGSS+D+
Sbjct: 688 YRRNFTDTNEYNIFAIS-ELGWVSEFALHVRNNGNGTLELGCHVVDVTSHIEEGSSVDRR 746

Query: 425 AAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTP EG-KILEEWFGRTI 483
A +R+++V++ QK+V +LP+ +EL SL P + T SV++ L +I W G +
Sbjct: 747 ARKRSSAVFMPQKLVNLLPQSFNDEL-SLAPGKESATLSVYTLDSSTLRIKSTWVGEST 805

Query: 484 IRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFV 543
I LS + + S + + IA+ +R
Sbjct: 806 ISPSNLSLEQLDEKL-----STGSPTS YLSTVQEIARSFYARRIN 846

Query: 544 D-GALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQ 602
D A L L'L +LD E + +I + ++ E N VA KI+ +
Sbjct: 847 DPEATLLPTLSLLES LDDEK-VKVDLNLIDRTLGFVVINEIKRKVNSTVAEKIYTKLGDL 905

Query: 603 ALLRRHPPPQTKMLS DLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNM 662
ALLRR P ++ + G D ++A L K + K DD R + +
Sbjct: 906 ALLRRQMOP IATKMASFRKKIQNF GYNFDTNTADELIKGV LKIKDDD---VRVGIEILL 961

Query: 663 YSRPMQMALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIRRFADVIVHRL LAAALGYSEQ 722
+ + M A YF +G + D +Q+ HYALN+P+YTHFT+P+RR+AD +VHR L A + +
Sbjct: 962 F-KTMPRARYFIAGKV-DPDQYGHYALNLP IYTHFTAPMRRYADHV VHRQLKAVI--HDT 1017

Query: 723 PDVEP-DTLQKQADHCNDRRMASKRVQELS IGLFFAVLVKE----SGPLESEAMVMGV LN 777
P E + L+ +++CN ++ + + QE +I L + + +G L + A V+ V
Sbjct: 1018 PYTEDMEALKITSEYCNFKKDCAYQAQEQAIHLL LCKTINDMGNTTGQLLT MATVLQVYE 1077

Query: 778 QAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEP 820
+FDV + FG++KR++ + L L F G L L W+P
Sbjct: 1078 SSFDVFIPEFGIEKRVHGDQLPLIKAED--GTNRVLELHWQP 1118

>gi|15616115|ref|NP_244420.1| ribonuclease R; virulence-associated protein
[Bacillus halodurans]
gi|25298858|pir||A84094 virulence-associated protein BH3553 [imported] -
Bacillus
halodurans (strain C-125)
gi|10176177|dbj|BAB07272.1| ribonuclease R [Bacillus halodurans]
Length = 771

Score = 214 bits (545), Expect = 5e-54
Identities = 163/515 (31%), Positives = 250/515 (48%), Gaps = 47/515 (9%)

Query: 232 KVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRP 291
KV+ ILE R + ++ D + Y L D R+P + + Q +
Sbjct: 127 KVIRILE---RGVSEVIGTYVDHQT-----YGLVVADDKRIPNDILIVNPEAQGLVDGH 177

Query: 292 KDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLE 351
K I +I + E A G++ LG + + I+ +YG+ F EVL+
Sbjct: 178 K-----VIVKITKYPEGRMSAEGEVISILGHKNDPGMDILSIYKYGIP-QAFPEEVLQ 230

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411
Q++P I E+ RRDLR + + TID + A+DLDDA+ RL +G F++GVHIADV
Sbjct: 231 -QAQNIPDEIDAGEIKNRRDLRDEPLVTIDGADAKDLDDAVHVSRLPNGNFKLGVHIADV 289

Query: 412 SYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPE 471
SY+V E S +D AAER TSVYLV +V+PM+P L +CSLNP D+LT S ++T +
Sbjct: 290 SYYVKEKSPIDLEAAERGTSVYLVDRVIPMIPHRLSNGICSLNPQVDRLTLSCEMEITRD 349

Query: 472 GKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLH 531
G+++ ++IR+ ++Y ++ +EE
Sbjct: 350 GQVVNHEIFQSVIRTNERMTYHDVNKILVEKEEELRNRYELLVPMFEDMEE----- 400

Query: 532 SIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAV 591
+A LR++RF GA+ D K A L E G P I E + KL+EEFML AN V
Sbjct: 401 -LAAILRKKRFRGAIDFD-FKEAKVLVDEEGKPSDVVIRERGVAEKLIEEFMLAANETV 458

Query: 592 AHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMGDPMDVSSAGALNKSLTKTFGDDKY 651
A F + R H P ++ L +EF G + ++ ++L K ++
Sbjct: 459 AEH-FHWLKLPMFYRIHEDPDSEKLGRFLEFITNFGYVVRGTANTVHPRALQKLL-EEVR 516

Query: 652 SLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHR 711
++V++ + R MQ A Y D H+ L+ YTHFTSPIRR+ D+IVHR
Sbjct: 517 GEPEEQVISTVMLRSMQQAKY-----DPTSLGHFGLSTEFYTHFTSPIRRYPDLIVHR 569

Query: 712 LLAAALGYSEQPDVEPDTLQKQ-----ADHCND 739
L+ Y + +V+ +T +K A HC++
Sbjct: 570 LIRE---YLIKGNVDEETQEKWRERLPEIARHCSE 601

>gi|23099883|ref|NP_693349.1| ribonuclease R [Oceanobacillus iheyensis]
gi|22778114|dbj|BAC14384.1| ribonuclease R [Oceanobacillus iheyensis]
Length = 744

Score = 209 bits (533), Expect = 1e-52
Identities = 140/418 (33%), Positives = 214/418 (51%), Gaps = 22/418 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359
I RI + E N A G++ LG + + I+ ++G+ DF +VLE Q P
Sbjct: 183 IARISKYPEGRNSAEGEIIHILGHKNDPGIDILSIHKGHIQV-DFPEDVLE-QAQQOTPE 240

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGS 419
I PDE+ RRDLR + I TID + A+DLDDA+ ++L++G +++GV+IADVS++V E S

Sbjct: 241 EIHPDEINGRRDLRNETIVTIDGADAKDLDDAVTVKKLSNGNYKLGVIYIADVSHYVKEES 300

Query: 420 SLDKVAERATSVYLVQKVPMPLPRLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 479
 +D+ A ER TSVYLV +V+PM+P L +CSLNP D+LT ++ +G+++E

Sbjct: 301 PIDREALERGTSVYLVDRVIPMIPHRLSNGICSLNPKVDRLTLGCMEINHQQQVVEHEI 360

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXXSVVEEVHQAVLNLSIAKQLRR 539
 +++I S +++Y ++ + +E NL SI LR

Sbjct: 361 FQSVIHSTERMTYSDVNKILVDQDEELRDKYEPLVPMFEEME-----NLASI---LRE 410

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMMLLANMAVAHKIFRTF 599
 +RF GA+ D K A L + G P I E + +L+EEFML AN +A F

Sbjct: 411 KRFGRGAIDFD-FKEAQVLVDDMGRPTDVAIRERSVAERLIEEFMLAANETIAEH-FHWM 468

Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS�TKTFGDDKYSLARKEVL 659
 + R H P L +F +G+ + +AG ++ + D + ++

Sbjct: 469 DVPFIHRIHEEPDEGKLEKFFDFLAGLGISVK-GTAGDIHPQELQKVIDSIRGEPEEMIV 527

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAAL 717
 + + R MQ A Y D + H+ L YTHFTSPIRR+ D+IVHRL+ L

Sbjct: 528 SKLMLRSMQAKY-----DPQSIGHFGLATDFYTHFTSPIRRYPDLIVHRLIRTYL 578

>gi|21673344|ref|NP_661409.1| ribonuclease II family protein [Chlorobium
 tepidum TLS]

gi|21646438|gb|AAM71751.1| ribonuclease II family protein [Chlorobium
 tepidum TLS]

Length = 720

Score = 208 bits (529), Expect = 4e-52
 Identities = 155/466 (33%), Positives = 233/466 (50%), Gaps = 57/466 (12%)

Query: 265 LFSPSDHRV-PRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQ 323
 L P ++ P I++PLK + K A L + ++ + LG

Sbjct: 154 LLKPDQRKILPEIHIPLKAAKAKAG-DKVLAGELEFLK-----SGTIQARVIEILGT 205

Query: 324 AGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPS 383
 AGE + E I G+D F E+L + + I +++ +R D+R +FTIDP

Sbjct: 206 AGESQVEVSAIARGLGID-ETFEPELL-TFAEKVREAITDEDLKERLDIRDKDVFTIDPV 263

Query: 384 TARDLDDALACRRLTD-GTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMPL 442
 A+D DDAL+ L + G ++VGVHIADVS++VPE S+LDK A +RATSVYLV +V+PML

Sbjct: 264 DAKDFDDALSIETLGNGGGYKVGVIADVSHYVPENSALDKEARKRATSVYLVDRVIPML 323

Query: 443 PRLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRRTIIRSCTKLSYDHAQSMIENX 502
 P L E++CSLNP D+L FSV + +T +G++ + F +T+I S + +Y+ Q +++

Sbjct: 324 PSRLSEKVCSLNPGVDRLAFSVFFNITKKGEVTKFEFHKTVIHKKRRFTYEDVQQILDAG 383

Query: 503 XXXXXXXXXXXXXXXXSVVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHET 562
 + + + L ++K++R QR G L + ++ F L

Sbjct: 384 KG-----DYFRELOALDQLSKKIRAQRMESGGLEFETEEVRFKLG-SN 425

Query: 563 GLPQGCHIYEYRDSNKLVEEFMMLLANMAVAHKIFRTF-----PEQALLRRHPPPQTKML 616
 G P E DS++L+EEFMMLLAN VA + + P + R H PQ + +

Sbjct: 426 GEPVEVIKKERLDSHRLIEEFMMLLANRTVAAYLTARYAENEKNPHPVIYRVHGAPQMEKV 485

Query: 617 SDLVEFCDQMGLPMDVSSAG-----ALNKS�TKTFGDDKYSLARKEVLTNMYSRPM 667
 L F ++G + + G AL + L K G + L + VL R M

Sbjct: 486 QVLASFVRKIGFDLKLDRKGKDSATVSSKALRELLQKVRGTNVEFLVNELVL-----RSM 540

Query: 668 QMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713
 A+Y L D H+ L YTHFTSPIRR+ D+IVHR+L

Sbjct: 541 SKAVY---SPLNDG---HFGLGFEHYTHFTSPIRRYPDLIVHRL 579

>gi|15672924|ref|NP_267098.1| ribonuclease [Lactococcus lactis subsp.
 lactis]

gi|18202798|sp|Q9CH00|RNR1_LACLA Ribonuclease R 1 (RNase R 1) (VacB
protein homolog 1)
gi|25298855|pir||F86742 ribonuclease [imported] - Lactococcus lactis
subsp. lactis (strain
IL1403)
gi|12723878|gb|AAK05040.1|AE006328_8 ribonuclease [Lactococcus lactis
subsp. lactis]
Length = 817

Score = 206 bits (525), Expect = 9e-52
Identities = 137/421 (32%), Positives = 223/421 (52%), Gaps = 27/421 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374
G + + +GQA + + +L + S+F EVL+ +++P +P +E+ R D R
Sbjct: 207 GLVTEIIGQADDQGIDVLEVLASMDI-VSEFPKEVLD-QAEAVPEEVPENEIVGRVDYRN 264

Query: 375 DCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYL 434
+ FTID + A+DLDDA+ +RL +G +E+GVHIADVS++V E S LDK A ER TSVY+
Sbjct: 265 EITFTIDGADAKDLDDAVHAKRLENGNYELGVHIADVSHYVTENSPLDKEAYERGTSVYV 324

Query: 435 VQKVVPMLPRLLCCELCSLNPMPTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDH 494
+VVPMLP L +CSLNP ++LT S + +++PEG+++ ++II++ +++YD
Sbjct: 325 TDRVVPMLPERLSNGICSLNPRINRLTQSCVMEISPEGRVINYQISQSIKTTERMTYDA 384

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKL 554
MI + + + ++ LH I + +R++R GA+ D ++
Sbjct: 385 VNQMIAGDEAALENYA-----KIADSVKIMVELHHILEAMRKRR---GAIDFDTVE- 432

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTK 614
A + +E GLP + +++E FML AN VA F + R H P+
Sbjct: 433 AKIIVNEKGLPIEIRKTRGIAERMIESFMLEANETVATH-FEAHGLPFIYRIHEQPKAD 491

Query: 615 MLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFC 674
L ++F G+ ++ +S G +++ + + F + VL+ M R MQ A Y
Sbjct: 492 RLQRFIDFAATFGMQIEGTSNG-IDQKVLQAFMKKIKGQPGEMVLSTMLLRSMQQARY-- 548

Query: 675 SGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQA 734
+ H+ L YTHFTSPIRR+ D++VHRL+ +G + P + LQK
Sbjct: 549 -----SENNEGHFGLAAENYTHFTSPIRRYPDLLVHRLI-REIGEGKTP---ANILQKWE 599

Query: 735 D 735
D
Sbjct: 600 D 600

>gi|21754656|dbj|BAC04542.1| unnamed protein product [Homo sapiens]
Length = 750

Score = 205 bits (521), Expect = 3e-51
Identities = 133/383 (34%), Positives = 197/383 (51%), Gaps = 32/383 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + QDF + RI W+ + G + LG
Sbjct: 366 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 415

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F
Sbjct: 416 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEEQKRKDLRKSHLVF 475

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 476 SIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 535

Query: 439 VPMLPRLLCCELCSLNPMPTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 536 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEAAQE 595

Query: 498 MIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553
 +++ S +EE+ A+ L IA+ +R +R GAL L+ ++
 Sbjct: 596 LLDGNLSVVDDIPEFKDLGEKSRQAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 655

Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
 + LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H
 Sbjct: 656 VCVQLDDKKNHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 709

Query: 609 PPPQTKMLSDLVEFCDQMGLPMD 631
 PPP + S+L E G +D
 Sbjct: 710 PPPHQEFFSELRECAKAKGFFID 732

Score = 59.3 bits (142), Expect = 3e-07
 Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101
 + ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A
 Sbjct: 225 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKDSDLVSDILIHGMKA 284

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
 RNR+++GD+VVV+LLP+++WK
 Sbjct: 285 RNRSIHGDVVVVVELLPKNEWKG 306

>gi|23020108|gb|ZP_00059814.1| hypothetical protein [Clostridium
 thermocellum ATCC 27405]
 Length = 757

Score = 203 bits (516), Expect = 1e-50
 Identities = 153/510 (30%), Positives = 245/510 (48%), Gaps = 50/510 (9%)

Query: 232 KVVYILEKK--HSRAATGILKLLADKNSDLF-----KKYALFSPSDHRVP-RIYVPLK 281
 +V+ + KK RA I+K++ N + K + P D R+ I++
 Sbjct: 108 RVIARINKKGIGDKRAEGEIIKIVKRANKTVVGTFESSKYFGFVVPDDPRISGDIFI--- 164

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGV 341
 P+D + K + + I+ W E A G++ +G E + I+ Y +
 Sbjct: 165 --PKDEINGAK--SGQKVVAEIVVWPEKRRNAEGRIIEIIGDKDEPGSDILSIKAYNLR 220

Query: 342 FSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGT 401
 DF EV+ +S+ T+ D + RRDLR + TID A+DLDDA++ RL +G
 Sbjct: 221 -EDFP EEVIR-EAKSISQTVTEDIKGRDLRDLTMVTIDGEDAKDLDDAVSIERLPNGN 278

Query: 402 FEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLT 461
 + +GVHIADVSY+V EGS LDK A +R TSVYLV +V+PM P+ L +CSLNP D+L
 Sbjct: 279 YRLGVHIADVSYVKEGSPLDKEALKRGTSVYLVDRVIPMFPEKELSNGLCSLNPKVDRLA 338

Query: 462 FSVIWKLTPGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVE 521
 F+V+ ++ G++++ ++I +++Y ++E H+++
 Sbjct: 339 FTVMEIDKSGRVVDHEIFESVINVNERMTYTDVYKILEENDEGLIERKYLCDTFHTMK 398

Query: 522 EVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVE 581
 E +A LR++R GA+ + + LD E G+P YE +N ++E
 Sbjct: 399 E-----LALILRKKRMDRGAI DFNFDEAKIVLD-EKGVPIEVKRYEMTIANNIE 447

Query: 582 EFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS 641
 EFML+ N VA F T + R H P + EF +G + +NK
 Sbjct: 448 EFMLVCNETVAEHFFWT-NTPFVYRIHEDPDPDKIEAFSEFVHNLGYTLK-----GINKI 501

Query: 642 LTKTFGD--DKYSLARKE-VLTNMYSRPMQMALY--FCSGMLQDQEQFRHYALNVPLYTH 696
 K D +K ++E +++ + R +Q A Y SG H+ L Y H
 Sbjct: 502 HPKALQDVLEKARGTKEETIISTVMLRSLQKARYSHINS-----HFGLAAKYCH 552

Query: 697 FTSPIRRFAADVIVHRLLAALGYSEQPDVE 726

FTSPIRR+ D+I+HR++ L + P+ E
Sbjct: 553 FTSPIRRYPDLIIHRIMKEYLKGTVPNPERE 582

>gi|16801605|ref|NP_471873.1| similar to exoribonuclease RNase-R [Listeria innocua]

gi|25298866|pir||AB1750 exoribonuclease RNase-R homolog lin2543 [imported]
- Listeria

innocua (strain Clip11262)

gi|16415065|emb|CAC97770.1| similar to exoribonuclease RNase-R [Listeria innocua]

Length = 793

Score = 201 bits (512), Expect = 3e-50

Identities = 138/430 (32%), Positives = 219/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDL 372
A G + +G + + I+ ++G+ + F EV+E + ++ P + ++G RRDL

Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISIA-FPEEVMEQVSKA-PDVVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSV 432
R I TID + A+DLDDA+ ++L +G +++GVHIADV+++V EGS LDK A +R TSV

Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNGNWKLGVHIADVTHYVTEGSPLDKEAQDRGTSV 312

Query: 433 YLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTTIIRSCTKLSY 492
YL V +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y

Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHVVNHEIFESIKTTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQL 552
++ +++ +A+ LRR+R GA+ D

Sbjct: 373 TDVNDILVEKDEALREKYAPIVPMLEAMQH-----LAEILRRKREKRGIDFD-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPO 612
K A + E G P+ + E L+EEFML AN VA F + R H P+

Sbjct: 422 KEARVVVDEEGHPPEEVVMRERSAGEHLIEEFMLAANETVAEH-FHWMDVPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKSILTKTFGDDKYSLARKEVLTNMYSRPMQMALY 672
L+ EF GL + K +D + A ++VL + +P +M +

Sbjct: 481 EDKLARFFEFITNFGL-----IVKGTANDIHPAALQQVLEEVKGKPEEMVV- 526

Query: 673 FCSGMLQDQEQFR-----HYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDV 725
+ ML+ +Q + H+ L+ YTHFTSPIRR+ D+IVHRL+ Y DV

Sbjct: 527 -STVMLRSMQQAKYDTVSAGHFGLSTDFYTHFTSPIRRYPDLIVHRLIRE---YLINGDV 582

Query: 726 EPDTLQKQAD 735

P+TL+K+A+

Sbjct: 583 RPETLEKRAE 592

>gi|16804487|ref|NP_465972.1| similar to exoribonuclease RNase-R [Listeria monocytogenes EGD-e]

gi|25298867|pir||AI1380 exoribonuclease RNase-R homolog lmo2449 [imported]
- Listeria

monocytogenes (strain EGD-e)

gi|16411937|emb|CAD00527.1| similar to exoribonuclease RNase-R [Listeria monocytogenes]

Length = 793

Score = 200 bits (509), Expect = 7e-50

Identities = 138/430 (32%), Positives = 218/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDL 372
A G + +G + + I+ ++G+ F EV+E + ++ P + ++G RRDL

Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISIG-FPEEVMEQVSKA-PDLVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSV 432
R I TID + A+DLDDA+ ++L +G +++GVHIADV+++V EGS LD A ER TSV

Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNGNWKLGVHIADVTHYVTEGSPLDIEAQERGTSV 312

Query: 433 YLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRRTIIRSKTSLY 492
 YLV +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y

Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHVVNHEIFESIKTTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQL 552
 ++ +++ ++A+ LRR+R GA+ D

Sbjct: 373 TDVNDILVEKDEALREKYAPIVPMLEAMQ-----NLAEILRRKREKRGIDFD-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQ 612
 K A + E G P+ + E L+EEFML AN VA F + R H P+

Sbjct: 422 KEARVVVDEEDGHPEAVVMRERSAGEHLIEEFMLANETVAEH-FHWMDVPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKSLLTKTFGDDKYSLARKEVLTNMYSRPMQMALY 672
 L+ EF GL + K +D + A ++VL + +P +M +

Sbjct: 481 EDKLARFFEFITNFG-----IVKGTANDIHPAALQQVLEEVKGKPEEMV- 526

Query: 673 FCSGMLQDQEQFR-----HYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDV 725
 + ML+ +Q + H+ L+ YTHFTSPIRR+ D+IVHRL+ Y DV

Sbjct: 527 -STVMLRSMQQAKYDTVSAGHFGFLSTDFYTHFTSPIRRYPDLIVHRLIRE---YLINGDV 582

Query: 726 EPDTLQKQAD 735
 P+TL+K+A+

Sbjct: 583 RPETLEKRAE 592

>gi|21397569|ref|NP_653554.1| RNB, RNB-like protein [Bacillus anthracis A2012]

Length = 808

Score = 197 bits (501), Expect = 7e-49
 Identities = 133/414 (32%), Positives = 214/414 (51%), Gaps = 22/414 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359
 + +I + E+ A G++ + LG + + ++ ++ + + F EV+E S+P

Sbjct: 185 VVKITSYPENRLSAEGEVIQILGHKNPDGVDILSVIHKHHLPLA-FPEEVME-HANSVPE 242

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSYFVPEGS 419
 TI +++ RRDLR I TID + A+DLDDA+ +L +G +++GVHIADVS++V EGS

Sbjct: 243 TISEEDLKDRDLRDQMIVTIDGADAKDLDDAVTVTKLENGNYKLGVIADVSHYVQEGS 302

Query: 420 SLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWF 479
 +D AAERATSVYLV +V+PM+P L +CSLNP D+LT S ++ G'+++

Sbjct: 303 PIDVEAAERATSVYLVDRVIPMIPHRLSNGICSLNPKVDRLTLSCEMEINNLDVVKHEI 362

Query: 480 GRTIIRSKTSLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLAKQLRR 539
 +++I++ +++Y +S++E+ E + + +A+ LR

Sbjct: 363 FQSVIKTTERMTYADVRSILEDEDEELMKRY-----EPLVPMFKEMGQLAQILRE 412

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599
 +R GA+ D K A L E G P + + S KL+EEFML+AN VA F

Sbjct: 413 KRMRRGAIDFD-FKEAKVLVDEEGKPTDVVMRDRSVSEKLIIEFMLVANETVAEH-FHWM 470

Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLLTKTFGDDKYSLARKEVL 659
 + R H P+ L EF G + + ++L + + + V+

Sbjct: 471 NVPFMYRVHEDPKEDKLERFFEFVTNFGYAVKGRANEVHPRALQQIL-EMVQGQPEEVVI 529

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713
 + + R M+ A Y D + H+ L+ YTHFTSPIRR+ D IVHRL+

Sbjct: 530 STVMLRSMKQARY-----DADSLGHFGFLSTEFYTHFTSPIRRYPDTIVHRLI 576

>gi|16080414|ref|NP_391241.1| similar to hypothetical proteins [Bacillus subtilis]

gi|7674332|sp|O32231|RNR_BACSU Ribonuclease R (RNase R) (VacB protein homolog)

gi|7443068|pir|G70027 conserved hypothetical protein yvaJ - Bacillus subtilis
gi|2635874|emb|CAB15366.1| similar to hypothetical proteins [Bacillus subtilis]

Length = 779

Score = 195 bits (495), Expect = 3e-48
Identities = 131/418 (31%), Positives = 213/418 (50%), Gaps = 22/418 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359
+ ++ + E A G++ LG + + ++ ++G+ +F ++ +E S P
Sbjct: 181 VVKLTSYPEGRMNAEGEVETILGHKNDPGIDILSVIHKHGLP-GEFPADAME-QASSTPD 238

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRRLTDGTFEVGVHIADVSYFVPEGS 419
TI ++ RRDLR I TID + A+DLDDA+ +L DG++++GVHIADVS++V E S
Sbjct: 239 TIDEKDLKDRRDLRDQVIVTIDGADAKDLDDAVTVTKLDDGSYKLGVHIADVSHYVTENS 298

Query: 420 SLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 479
+DK A ER TSVYLV +V+PM+P L +CSLNP D+LT S + +G++ E
Sbjct: 299 PIDKEALERGTSVYLVDRVIPMIPHRLSNGICSLNPKVDRLTLSCEMTINSQGQVTEHEI 358

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRR 539
+++I++ +++Y ++ + E + ++ +A+ LR
Sbjct: 359 FQSVIKTTERMTYSVDNKKILVD-----DDEELKQKYEPLVPMFKDIMERLAQILRD 408

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599
+R GA+ D K A L + G + I E + KL+EEFML+AN VA F
Sbjct: 409 KRMDRGAVDFD-FKEAKVLVDDEGAVKDVIRERSVAEKLIEEFMLVANETVAEH-FHWM 466

Query: 600 PEQALLRRHPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVL 659
+ R H P + L +EF G + +AG ++ ++ D + V+
Sbjct: 467 NVPFIYRIHEEPNAEKLQKFLEFVTTFGYVVK-GTAGNIHPRALQSILDAVRDRPEETVI 525

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAAL 717
+ + R M+ A Y D + H+ L+ YTHFTSPIRR+ D+IVHRL+ L
Sbjct: 526 STVMLRSMQAKY-----DPQSLGHFGLSTEFYTHFTSPIRRYPDLIVHRLIRTYL 576

>gi|15894003|ref|NP_347352.1| FUSION ribonuclease and ribosomal protein S1 domain [Clostridium

acetobutylicum]

gi|25298861|pir|A96988 FUSION ribonuclease and ribosomal protein S1 domain [imported] -

Clostridium acetobutylicum

gi|15023595|gb|AAK78692.1|AE007586_9 FUSION ribonuclease and ribosomal protein S1 domain [Clostridium

acetobutylicum]

Length = 730

Score = 190 bits (483), Expect = 7e-47
Identities = 128/420 (30%), Positives = 213/420 (50%), Gaps = 35/420 (8%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359
+ I W + G++ + +G GE + I+ ++ + E +E + +P
Sbjct: 177 VAEITVWPKKRRNPEGKIVEIIGSKGEKGV DILTIIKKH--KLPEKFPEKVERFAEGIPN 234

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRRLTDGTFEVGVHIADVSYFVPEGS 419
IP E +RRD+R + TID A+DLDDA++ +L++G F++GVHIADVS +V E +
Sbjct: 235 EIPSEYKRRRDIRDVKMVTIDGEDAKDLDDAVSIEKLSNGNFKLGVHIADVSNYVREDN 294

Query: 420 SLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 479
LDK A +RATSVYL+ +V+PMLP+ L +CSLNP D+L S ++ P GK+++
Sbjct: 295 PLDKALKRATSVYLIDRVIPMLPKKLSNGICSLNPRQDRLAMSCFMEIDPTGKVIQHEI 354

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRR 539
+II++ +++Y ++ + + E ++ N+ +A L +

Sbjct: 355 FESIIKTNERMTYTDVTKILRD-----HDEETIKAFEYLYDDFKNMEELASILNK 404

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVA-HKIFRT 598
 +R + GA+ D + TL+ E G P YE +N+++EEFML+ N +A H +

Sbjct: 405 KRLLRGALDFDFEESKITLN-ELGKPVEVKPYERAVANRIIEEFMLVCNETIAEHFYWAN 463

Query: 599 FPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSS---AGALNKSLTKTFGDDKYSLAR 655
 P + R H P ++ L EF +G + S L + K G +

Sbjct: 464 IP--FVYRVHEEPDSEKLERFNEFIHNLGYAVRWGSEVHPKQLQDVIEKIKGKKE----- 516

Query: 656 KEVLTNMYSRPMQMALYF--CSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713
 + V++ + R ++ A Y CSG H+ L Y HFTSPIRR+ D+I+HR++

Sbjct: 517 ETVVSTLLLRSLKQARYSPECSG-----HFGLAARYYCHFTSPIRRYPDLIIHRIM 567

>gi|27467483|ref|NP_764120.1| ribonuclease R [Staphylococcus epidermidis ATCC 12228]
 gi|27315026|gb|AAO04162.1|AE016745_261 ribonuclease R [Staphylococcus epidermidis ATCC 12228]
 Length = 792

Score = 190 bits (483), Expect = 8e-47
 Identities = 132/430 (30%), Positives = 215/430 (50%), Gaps = 26/430 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374
 G ++ LG + + I+ ++G++ +F +VL+ + +P I P E+ RRDLR

Sbjct: 199 GHVSAILGHKNDPGVDILSIIYQHIGIEI-EFPDDVLQ-EAEEVPDVIEPSEIEGRDLRD 256

Query: 375 DCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYL 434
 + TID + A+DLDDA+A ++L +G E+ V IADVS+V EGS+LDK A +RATSVYL

Sbjct: 257 ELTITIDGADAKDLDDAIAVKKLKNGNTELTVSIADVSYVKEGSALDKEAYDRATSVYL 316

Query: 435 VQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRRTIIRSCTKLSYDH 494
 V +V+PM+P L +CSLNP D+LT S ++ G++++ ++I S +++YD

Sbjct: 317 VDRVIPMIPHRLSNGICSLNPEEDRLTLSCRMEINERGEVVKHEIFDSVIHSNYRMTYDA 376

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLIAKQLRRQRFVDGALRLDQLKL 554
 +I + ++ ++ +L R R G + D +

Sbjct: 377 VNKIITDQDSEIRSQYKDLTPMLDLAQD-----LSNRLIRMRKRGEIDFD-INE 425

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTK 614
 A L ++ G+P + E + +L+E FML AN VA F + R H P++

Sbjct: 426 AKVLVNDEGIPTTEVLMRERGEGERLIESFMLAANETVAEH-FNKLEVFPFIYRVHEQPKSD 484

Query: 615 MLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFC 674
 L +F G+ M + ++ + + ++ + V++ M R MQ A Y

Sbjct: 485 RLRQFFDFITNFGI-MIKGTGEDIHPTTLQNIQEEVEGRPEQMVISMTMLRSMQQAHY-- 541

Query: 675 SGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVE----PDTL 730
 D H+ L+ YTHFTSPIRR+ D+ VHRL+ L + E +TL

Sbjct: 542 -----DDVNLGHFGLSAEYYTHFTSPIRRYPDLTVHRLIRKYLIENSMDKKEIRHWEETL 596

Query: 731 QKQADHCNDR 740
 + A+H + R

Sbjct: 597 PELAEHTSQR 606

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Jan 29, 2003 9:26 AM
 Number of letters in database: 423,161,544
 Number of sequences in database: 1,321,324

Lambda	K	H
0.319	0.136	0.399

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 681,347,984

Number of Sequences: 1321324

Number of extensions: 28649337

Number of successful extensions: 62317

Number of sequences better than 10.0: 242

Number of HSP's better than 10.0 without gapping: 232

Number of HSP's successfully gapped in prelim test: 10

Number of HSP's that attempted gapping in prelim test: 61354

Number of HSP's gapped (non-prelim): 402

length of query: 870

length of database: 423,161,544

effective HSP length: 132

effective length of query: 738

effective length of database: 248,746,776

effective search space: 183575120688

effective search space used: 183575120688

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 77 (34.3 bits)